

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 10:04:44 ; Search time 4254.07 Seconds
(without alignments)
4400.663 Million cell updates/sec

Title: US-09-325-019-1
Perfect score: 3658
Sequence: 1 cggacttaccacccagctcca.....aaaaaaaaaaaaaaaaaaaaa 3658

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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81: gb_pat1:*
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83: em_hcg0:*
84: gb_hcg24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2929.4	80.1	176767	63 AF192304	AF192304 Homo sapi
2	2613.4	71.4	2830	10 AF100779	AF100779 Homo sapi
3	920.8	25.2	5020	74 AB004873	AB004873 Mus muscu
4	815.4	22.3	1766	74 AF100777	AF100777 Mus muscu
5	585.4	16.0	138446	35 AC011160	AC011160 Homo sapi
6	422.8	11.6	69016	47 AC023088	AC023088 Homo sapi
7	243.4	6.7	2075	81 AR018957	AR018957 Sequence
8	243.4	6.7	2075	81 I11636	I11636 Sequence 1
9	243.4	6.7	2075	81 I32210	I32210 Sequence 1
10	243.4	6.7	2075	85 H0MCONGRO	H0MCONGRO Human conne
11	243.4	6.7	2312	69 HSCOTGF	HSCOTGF H. sapiens m
12	229.6	6.3	138446	35 AC011160	AC011160 Homo sapi
13	225.4	6.2	2338	74 AB023068	AB023068 Rattus no
14	225.4	6.2	2345	74 AF120275	AF120275 Rattus no
15	223.4	6.1	1496	3 S0U83916	S0U83916 Sus scrofa
16	220.4	6.0	2330	74 M0STGFB	M0STGFB Sus scrofa
17	219	6.0	1953	4 X043524	X043524 Xenopus lae
18	218.8	6.0	1585	4 NV1271167	NV1271167 Notopttha
19	218.8	6.0	2267	74 M0SF1P12B	M0SF1P12B Mouse FISP-
20	217	5.9	1598	3 U70060	U70060 Sus scrofa
21	207.8	5.7	2330	3 BTA000137	BTA000137 Bos tauru

22	199	5.4	1900	69	HSU14750
23	198	5.4	1212	10	AF100781
24	196.4	5.4	1973	69	HSNOVH
25	189.2	5.2	1065	74	MMNOVH
26	187.6	5.1	1064	74	MMNOVH
27	187.6	5.1	2380	74	MMNOVH
28	180.4	4.9	1068	10	AF143679
29	179	4.9	1305	74	AF171936
30	173.4	4.7	1927	4	CJUI3063
31	169.4	4.6	2078	4	XIU37063
32	167	4.6	1975	81	A28405
33	167	4.6	1975	81	A28444
34	167	4.6	1906	4	CGNOVNRNA
35	135.2	3.7	1875	4	CHCKEC
36	132	3.6	684	81	A28405
37	129.6	3.5	1283	10	AF083500
38	128.6	3.5	1303	10	AF074604
39	129.6	3.5	1427	10	AF0100780
40	126.4	3.5	1871	74	ABO15877
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42	124.4	3.4	2018	74	MUSCRR6.1A
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45	111.2	3.0	1935	10	AF003594
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					AF100781 Homo sapi
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					X97883 M.musculus
					T09237 M.musculus
					X96585 M.musculus
					AF143679 Homo sapi
					AF171936 Rattus no
					U13063 Coturnix ja
					U37063 Xenopus lae
					A28405 Sequence 1
					A28444 nov mRNA seq
					X59284 G.gallus no
					J04496 Chicken CEF
					A28405 Sequence II
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					AF003594 Homo sapi

ALIGNMENTS

[illegible]

RESULT	1	HTG	01-JUN-2000
LOCUS	AF192304	176767 bp	DNA
DEFINITION	Homo sapiens chromosome 8 map 8q24 clone CTC-45843, WORKING DRAFT		
SEQUENCE	SEQUENCE, 3 ordered pieces.		
ACCESSION	AF192304		
VERSION	AF192304.2	GI:8151747	
KEYWORDS	HTG; HTGS_PHASE2; HTGS_DRAFT.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1. (bases 1 to 176767)		
AUTHORS	Bleichschmidt,K., Baumgart,C., Dette,M.D., Jahn,N., Menzel,U., Polley,A., Reichwald,K., Schillabel,M.B., Schudy,A., Taudien,S., Wen,G., Kalaydjieva,L., Goodman,R., Gresham,D., Baas,F., Jonge,R. and Rosenthal,A.		
TITLE	Chromosome 8 genomic sequence		
JOURNAL	Unpublished		
REFERENCE	2. (bases 1 to 176767)		
AUTHORS	Bleichschmidt,K., Kalaydjieva,L., Goodman,R., Gresham,D., Baas,F., Jonge,R.d., Schillabel,M., Schatteroy,R., Dette,M., Menzel,U. and Rosenthal,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-OCT-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany		
REFERENCE	3. (bases 1 to 176767)		
AUTHORS	Genome Sequencing Center Jena.		
TITLE	Direct Submission		
JOURNAL	Submitted (24-MAY-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany		
REFERENCE	On Jun 1, 2000 this sequence version replaced gi:5651493.		
TITLE	* NOTE: This is a 'working draft' sequence. It currently		
JOURNAL	* consists of 3 contigs. Gaps between the contigs		
REFERENCE	* are represented as runs of N. The order of the pieces		
AUTHORS	* is believed to be correct as given, however the sizes		
TITLE	* of the gaps between them are based on estimates that have		
JOURNAL	* been provided by the submittor.		
REFERENCE	* This sequence will be replaced		
AUTHORS	* by the finished sequence as soon as it is available and		
TITLE	* the accession number will be preserved.		
JOURNAL	* 51879: contig of 51878 bp in length		
REFERENCE	* 51879: gap of unknown length		
AUTHORS	* 51879: 151896: contig of 99918 bp in length		

FEATURES		151897	151966: gap of unknown length	151997	176767: contig of 24771 bp in length.
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		15197. 176767			
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		clone_end:5P6			
		vector_side:right"			
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Best Local Similarity: 199.6%; Pred. No. 0;					
Matches 2936; Conservative, 0; Mismatches 11; Indels 0; Gaps					
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QY	758	cttcacacttgcggtctgcatcagacacgctctcatcaaccgaagtactgtgagttg	817		
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QY	878	tccttaattggctgtgctctctccgcgagagctcctatgattaaatgctgtcttctgtaact	937		
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DB	66234	GAGCTGTAGAAATCCCATGACATCTTTGCTACTTGGAAATCTTACCCGATTTCTCAGA	662933		
QY	998	aattgccaaactgagagagacaaatctctgtgtcttggagactaacccaatgctcgtgaag	1057		
DB	66294	AATTGCCAACTGAGCAGGACCAAAATCTTGGGCTTGGGGACTAATACCAATGCTGTGAAG	663533		
QY	1058	cagctagaccccttatgtcccaatacttccacacaatgagagcttaagttaacctgtatcgac	1117		
DB	66354	CAGTACAGCCCTTAATGGCCAAATCACTTTTCCCAATGAGGCTTAAGTTACCTCATCTGAGC	664133		
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QY	1298	gctggtatcttgactcaatcccaagaatgagaaatcaggtgagacttttaataatacaactt	1357		
DB	66594	GCTGGAATCTTGCTTAATTCCAAGAAATGGAATCAGGTAGACTTTTAATATCACTAATTT	666533		
QY	1358	ctctcttatgacccaacacacagagcctcttggtccatctcagatgaaatagatgaaatct	1417		
DB	66654	CTCTCTTATGATGCCAAACACAAAGACTCTTTTGGGTGCATTCAGATGAATATGATGAATTT	667133		
QY	1418	ggagacaatagataatctatatcttggagacctgtccagagagtaactgtlaattggaattct	1477		


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RESULT 3
AB004873 5020 bp mRNA ROD 25-FEB-1998
LOCUS Mus musculus; mRNA for ELM1, complete cds.
DEFINITION
ACCESSION AB004873.1 GI:2911143
VERSION ELM1; ELM1: expressed in low-metastatic cells.
KEYWORDS Mus musculus (sub species: C3H, strain: HeJ) melanoma
SOURCE cell_line: K-1735 M2 CDNA to mRNA, clone_11b: lambda zap II
clone: ELM1 R37.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sclurognathli; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5020)
AUTHORS Hashimoto, Y.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-1997) to the DDBJ/EMBL/GenBank databases.
Yasunobu Hashimoto, National Cancer Center Research Institute,
Biology Division, 1-1, Tsukiji 5-chome, Chuo-ku, Tokyo 104, Japan
(E-mail: yhashimoto@ncc.go.jp, Tel: 81-3-3542-2511,
Fax: 81-3-3542-0807)
REFERENCE 2 (sites)
AUTHORS Hashimoto, Y., Shindo-Okada, N., Tani, M., Nagamachi, Y., Takeuchi, K.,
Shirolishi, T., Toma, H., and Yokota, J.
TITLE Expression of the ELM1 gene, a novel gene of the CCN (connective
tissue growth factor, Cyr61/Cef10, and neuroblastoma overexpressed
gene) family, suppresses in vivo tumor growth and metastasis of
K-1735 murine melanoma cells
J. Exp. Med. 187 (3), 289-296 (1998)
98119879.

JOURNAL MEDLINE
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BASE COUNT	1341 a	1173 c	1145 g	1361 t
ORIGIN				

Query Match	25.2%;	Score 920.8;	DB 74;	Length 5020;
Best Local Similarity	60.9%;	Pred. No. 4.3e-209;		
Matches 1938; Conservative	0;	Mismatches 1092;	Indels 152;	Gaps 21.

[illegible]

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D	1949	AAAGGCGTAATGCTGCTGTGTGTGATGACGAATGATTTGAGAGATCTATTGCTTGC	2008
Q	1706	tgaggaaagccccagttat--actccagagacagagaaagtcaagccattcaagaag	1763
D	2009	AGGGAGATGATGACCTCAATTCATCCCGATGTGGGACAAAGGCCAACATCTTCAAG	2068
Q	1764	gacaaattgactctcaacagaaatgagctgctgacacgcaagagcttgaggcattgggca	1823
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D	2127	-----AAATGGGCT	2174
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OY	1944	agctttagagagaccagctctgcagacacatgcagaccactgtgaatagacacagagcgttc	2003
Db	2228	gcccccttgaagaagactcttttaagctctacgcgcacacttaacagaatttgcatccaacaa	2287
OY	2004	aggttaagggtgtgtgttcacaacccaagaagtgtgtgtcccttgtagcagccttgggtgacct	2063
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OY	2064	ctaaagcttggagagcgtgtgtggaactccagggcccccggtgttcaggagacacatctatgcaga	2123
Db	2336	agtgactgtggttaaggccacagatagttcccttgaccacagacaaatctttttgtttcagt	2395
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Db	3106	gggagacttgaaatttccctctcttctcctgcgaacttcccaaaagcccttgcttatgcaagcc	3165
OY	2959	atacaagtggtctcatctaatactctgtagatatacaggaagcgtgtgatgtgttctact	3013
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Query Match	Best Local Similarity	22.3%	Score 815.4	DB 74	Length 1766
Matches 1135	Conservative	0	Mismatches 436	Indels	Gaps 5
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Oy	3019	ttaatcagacgtctctcttcccaagctacacatgtaaaatagattttacagctcaaat	3078		
Db	3226	ttcctttagAACCCCTTTCTTCTCCAGGANTCTCATCTTAAAGTAAGAAATCTCTCTTAA	3285		
Oy	3079	tatatgaagtgctctagcaagaagacatttaattcacaagaatgatgatgta	3138		
Db	3286	GAGCGCTGATTTTGATTAACATATGTTGATATGTCGTAAAGACTTGATGTAATA	3345		
Oy	3139	ta 3140.			
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VERSION	AF100777.1	GI:4028576			
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FEATURES					
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ORIGIN					

Db 177 CTTCACCCGACACACTAGAGAAAGACTACAGCCCGAATTCGCAAGTGGCCATG 236
 QY 65 tgaatgacccgacatcccccacccgctgcccgtgggggttcagctccatcaagatgctg 124
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 QY 665 cctcaccgac 724
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 QY 785 acgctcctac 844
 Db 957 ACGCACTTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1016
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 Db 1077 GGTCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 1136
 QY 965 tctgctcctgac 1024
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RESULT 5
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 DEFINITION AC011160.2 GI:7341861
 ACCESSION AC011160.2 GI:7341861
 VERSION HTG: HTGS_PHASE0.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 138446)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Homo sapiens, clone RP11-9F9
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 138446)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
 Baldwin, J., Barna, N., Beckwith, R., Boguski, L., Bouckhagter, B.,
 Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
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 Teste, S., Tittell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
 Wyman, D., Ye, W., Zimmer, A. and Zody, M.

TITLE Direct Submission
 JOURNAL Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome
 Research, 920 Charles Street, Cambridge, MA 02141, USA
 COMMENT On Mar 30, 2000 this sequence version replaced g1:6006142.
 All repeats were identified using RepeatMasker:
 Smit, A.P. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/XK/RepeatMasker.html
 ----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L3009
Center clone name: 9_F_9

* NOTE: This record contains 152 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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Query Match 11.6%; Score 422.8; DB 47; Length 69016;
Best local similarity 94.4%; Pred. No. 4,4e-90;
Matches 472; Conservative 0; Mismatches 22; Indels 6; Gaps 3;

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DB 38740 ATTATGATTTGAAATATATATTTACTGTTGAAATCTTTATTAGGCCCTTT 38799
QY 2350 ctgtgcacagacacctctcaagtgcttgcatgtatagctcacatctcaacaa 2409
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REFERENCE	1 (bases 1 to 2075)
AUTHORS	Grotdorast,G.R. and Bradham,D.M., Jr.
TITLE	Treatment of cell proliferative disorders using antibodies which bind connective tissue growth factor
JOURNAL	Patent: US 5783187 A 1 21-JUL-1996;
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1 (bases 1 to 2075)	
Grondorf, G. R. and Bradman, D. M., Jr.	
Connective tissue growth factor (CTGF)	
Patent: US 5408040-A 1 18-APR-1995;	
Location/Qualifiers	
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ORIGIN	BASE COUNT				
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Best Local Similarity :	56.2%	Pred. No. 2.4e+47;		
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REFERENCE 1 (bases 1 to 2075)
AUTHORS Grotendorst, G. R. and Bradham, D. M. Jr.

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TITLE Polynucleotides encoding connective tissue growth factor
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Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3009
Center clone name: 9_F_9

* NOTE: This record contains 132 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
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Dd	797	CAACTGCTGTGTCACGACACACAGAGTGAAGCGCTGTTCTTAAGACTTGTGGATGGGAT	856
Oy	608	cttcaactggatctcaaatgttaagcccaagtgtgcgccttagcaagaagacgcgccttg	667
Dd	857	CTCCACCGGGGTATCAATGACAAATACCTTCTGCAAGCTGGAGAAGCAGAGTCTCTG	916
Oy	668	caacttgcgcctgacgtgtgtgaatcatcatcaactcaataagcagggaagaagtgtct	727
Dd	917	CATGTTAGCGCCCTGTGAAGCTGACCTAGAGAAAACATTAAAGAGGGCAAAATGTCAT	976
Oy	728	ggctgtgtaacacgcagaggcatcatgaacttcaacttgcgcatttcgggctgtcatagcaacg	787
Dd	977	CCGAGCGCTTAATAATTGGCAAGCCTGTCAAAATTGAGCTTTCTGGCTCACACAGTGTGA	1036
Oy	788	ctctcatcaaccaagactgtgagtttgatgagacataagttgtctcatccctcaaa	847
Dd	1037	GACCTACCGGGCTAAGTCTGTGGGGTGTGACAGGACGGCGCTGCTCACACCGCACAG	1096
Oy	848	gtctaagctctgcagcgtgtcttccatgttctcgtatgaggttggcttctccgcagagt	907

	Matches	505; Conservative	0; Mismatches	396; Indels	12; Gaps
QY	77	atccccccccccgctgccccgcgtggggtgacagctcaacagatgctgtgagctgttaa	136		
Db	332	AGCGGCGCCCGGCGTCCGCCCGCGGTGAGCTGTGCTGGAAGCGCTCGGCTGTCGCC	391		
QY	137	gattgtcgctacagagactgttggagacaactgcagagaggtctgcacatctgtgaacccccacg	196		
Db	392	CGTGTGCGCCCAAGAGAGTGGGAGAACTGTGCACGGAGCGTGTATCCCTCGACGCCACACAA	451		
QY	197	gggcctctacagtgctactcaagcgggagcccgcccgaggaagcaatagagatgtgtgcaca	256		
Db	452	GGGCTCTTCTTGCGCACT---TCGGCTCCCGCCCAACCGCAAGATTGACGTGTGACATGC	508		
QY	257	ggatgtcggtgttggggtcgctgcctctgatactgaggtgtgcgtcaacaacagcgagctctcca	316		
Db	509	CAAGATAGTGTACACCTCTGTCTTTCGTGGGTGCTGCTGTAACGGACAGCGGAGTCTTCCA	568		
QY	317	gactaactgcagaatcaacaactgcacgtgtcatgcagcgcgcggtgtggctgcacacacgtt-	375		
Db	569	AAGCAGTGTGCAAAATACCAAGTACACTTGCCTGGATGGGCGCGGTGGCTGTGTGCCCTGTG	628		
QY	376	--ggtccgagtgagcccccccggtctctgtgtgtcccccaccccgcgcggtgtgagatacc	433		
Db	629	CAGCATGAGACGTGCGCGCTCGCCAGCCCTGACTGCCCCCTTCCGAAAGAGGTAAAGTGC	688		
QY	434	tggcacactgcgtgtgtgtgaggtgtgtatgtgaag-----acgacgcgaagagcgacacga	487		
Db	689	CGGGAATAGCTGTGAGAGTGGGTGTGTGTGATGAGCCCAAGAGCCGACAGTGTGTGGCC	748		
QY	488	gaccgcagccccgtgaacacagagagccttcgatgtctgtgtgtgtgtgtgtgtgtgtgtgacag	547		
Db	749	TGCCCTACTCTGCTTACCCACTGGAAGACAAATTGGCCCTGACCCCACTATGATCTGAGC	808		
QY	548	gaactgtcatactcaacacagccccctgtgagccctctgtctcaacagctcgcgctgtgggt	607		
Db	809	CAACTGCTGTGTCCAGACACAGAGTGGAGCGCTGTCTTAAGACTGTGTGGATGTGGCAT	868		
QY	608	ctccactgtgattctccaaatgttaacgcgcccagttgtgcctgtgacgaagagagccgctctg	667		
Db	869	CTCCACCCGGGTATCCAAATGACAAATACCTTCTGCAAGGCTGGAGAAAGACAGATGCTCTCG	928		
QY	668	caactgtggcgaaatgcagatgtgtgacatccatacactttaagcagaggaagaggttct	727		
Db	929	CATGTCACGGCCCTGTGTGAAGCTGACCTAGAGGAAACATTAAAGAAAGGCAAAATGTGCAT	988		
QY	728	ggtctgtacacaggccagagagcatccatgaacttcaactctgcgcgtgtgcataagcacag	787		
Db	989	CCGAGCGGCTTAAATATGGCCAGCCGTGCAAGTTTGAAGTTTCTGTGGCTGCACCAAGTGTGA	1048		
QY	788	ctctcatcaaacccaagtctctgt	847		
Db	1049	GACCTACCGGCTTAAAGTTCTGTGGGGGTGTGCACGGACGGCCGCTCTGTGCACACCCGACAG	1108		
QY	848	gtctaaagacttcagagctgtctctccacagttgtctgtatgtgtgtgtgtgtgtgtgtgtgtgt	907		
Db	1109	AACACACACACTGCTCGTGAAGTTAAATGATGCCCGCATGGCGAGATCATGAATAAAGACAT	1168		
QY	908	cctatgatattatcgtctctctctgttaacctgtgagctgtgtagaaatcccaatgacatcttgc	967		
Db	1169	GATGTTCATCAAGACCTGTGCTGTGCATTACAACTGTCCCGGGACAAATGACATCTTTGA	1228		
QY	968	tgaacttgaaacac ⁹⁸⁰			
Db	1229	GTCCTTGTACTAC ¹²⁴¹			

RESULT 15

SSU83916

LOCUS

DEFINITION Sus scrofa connective tissue growth factor (CTGF) mRNA, complete cds.

ACCESSION U83916

1496 bp

mRNA

12-AUG-1997

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 10:15:19 ; Search time 152.1 Seconds
(without alignments)
9034.675 Million cell updates/sec

Title: US-09-325-019-1
Perfect score: 3658
Sequence: 1 cgcacttaccacccagctcca.....aaaaaaaaaaaaaaaa 3658

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N.Geneseq.36.*
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2: /SID56/gcgdata/geneseq/NA1981.DAT.*
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19: /SID56/gcgdata/geneseq/NA1998.DAT.*
20: /SID56/gcgdata/geneseq/NA1999.DAT.*
21: /SID56/gcgdata/geneseq/NA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3658	100.0	3658	21	Human connective t
2	2611.8	71.4	2830	20	Human WISP-1 clone
3	1193	32.6	1403	20	Human WISP-1 clone
4	1004.4	27.5	1101	20	Human WISP-1 clone
5	815.4	22.3	1766	20	Mouse WISP-1 clone
6	773.8	21.2	1202	20	Mouse WISP-1 clone
7	747.6	20.4	1140	20	Mouse WISP-1 clone
8	735	20.1	1183	20	Human WISP-1 clone
9	459.8	12.6	1101	20	Human WISP-1 clone
10	404	11.0	546	20	Human WISP-1 clone
11	403.4	11.0	683	20	Human WISP-1 clone
12	355.8	9.7	540	21	Human CTGF-4 relat

c	13	316.4	8.6	539	21	258615	Human CTGF-4 relat
	14	295.4	8.1	311	21	258616	Human CTGF-4 relat
	15	277.8	7.6	1062	21	211246	Human connective t
	16	255.2	7.0	693	20	276491	Human WISP-1 clone
	17	243.4	6.7	2075	16	T04226	Connective tissue
	18	243.4	6.7	2075	16	T45360	Human connective t
	19	243.4	6.7	2075	18	T51234	Connective tissue
	20	243.4	6.7	2075	19	V38085	Human connective t
	21	243.4	6.7	2075	20	X61317	Human connective t
	22	225.4	6.2	2338	20	X90030	Rat connective tis
	23	220.4	6.0	2330	13	Q26422	Gene for beta-IG-M
	24	218.8	6.0	2267	18	T94700	Murine Flsp12 cDNA
	25	199.6	5.5	1335	20	X76497	Human WISP-3 prote
c	26	199.6	5.5	1335	20	X76498	Human WISP-3 prote
	27	198	5.4	1142	20	211245	Human connective t
	28	198	5.4	1183	21	A06928	Human growth facto
	29	198	5.4	1212	20	X76499	Human WISP-3 prote
c	30	183.4	5.0	1212	20	X76500	Human WISP-3 prote
	31	183.4	5.0	197	21	258617	Human CTGF-4 relat
	32	167	4.6	1975	14	Q36031	Chicken nov coding
	33	154.6	4.2	484	21	258618	Human CTGF-4 relat
	34	130.4	3.6	684	14	Q36032	Chicken nov gene f
	35	129.6	3.5	738	20	X76501	Human WISP-2 prote
c	36	129.6	3.5	750	20	X76487	Human WISP-2 prote
	37	129.6	3.5	1257	20	X28435	ECF-like homologue
	38	129.6	3.5	1266	21	A30048	Human PRO261 nucle
	39	129.6	3.5	1285	19	V29260	Human connective t
	40	129.6	3.5	1293	20	X76486	Human WISP-2 prote
	41	129.6	3.5	1522	20	X16595	Human growth facto
	42	124.4	3.4	2028	13	Q26421	Gene for beta-IG-M
	43	123.6	3.4	841	21	X76502	Human WISP-2 prote
	44	120.8	3.3	531	21	A06931	Human growth facto
	45	111.6	3.1	236	21	258619	Human CTGF-4 relat

ALIGNMENTS

RESULT	1	
ID	258613	standard; CDNA: 3658 BP.
AC	258613:	
XX		
DT	11-APR-2000	(first entry)
DE	Human connective tissue growth factor-4 (CTGF-4) encoding CDNA.	
XX		
KW	Connective tissue growth factor-4; CTGF-4; human; immune system disorder;	
KW	hematopoietic disorder; autoimmune disorder; diabetes mellitus; asthma;	
KW	respiratory disorder; inflammation; hyperproliferative disorder;	
KW	infection; central nervous system disease; Alzheimer's disease; AIDS;	
KW	food additive; ss.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	3..4010
FT		/*tag a
FT		/product- "CTGF-4"
XX		
PN	W09962927-AL	
XX		
PD	09-DEC-1999.	
XX		
PF	03-JUN-1999.	99MO-US12150.
XX		
PR	05-JUN-1998.	98US-0088320.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Ruben SM, Young PE;	
XX		

DR WPI, 2000-147042/13.
DR P-SDS; Y59247.
XX
PT New isolated connective tissue growth factor-4, used for treating e.g.
PT cancers -
XX
PS Claim 4; Fig 1A-E; 196pp; English.

XX
CC The invention provides an isolated human connective tissue growth factor
CC -4 (CTGF-4) polypeptide. The CTGF-4 cDNA is deposited under ATCC No.
CC 209816. The CTGF-4 protein can be expressed by standard recombinant
CC methodology. The polypeptides can be used for preventing, treating or
CC ameliorating a medical condition. They may be useful in treating
CC deficiencies or disorders of the immune system, by activating or
CC inhibiting the proliferation, differentiation, or mobilization
CC (chemotaxis) of immune cells, treating or detecting deficiencies or
CC disorders of hematopoietic cells (e.g. blood protein disorders, ataxia
CC telangiectasia, HIV infection, Di George syndrome, anemia or
CC thrombocytopenia), to modulate hemostatic (the stopping of bleeding) or
CC thrombolytic activity (clot formation) (e.g. blood coagulation disorders,
CC blood platelet disorders, or wounds resulting from trauma, or surgery),
CC in treating or detecting autoimmune disorders (e.g. Addison's disease,
CC rheumatoid arthritis, allergic encephalomyelitis, Goodpasture syndrome,
CC multiple sclerosis, purpura, Reiter's disease, Guillain-Barre syndrome,
CC systemic lupus erythematosus, insulin dependent diabetes mellitus or
CC autoimmune inflammatory eye disease), treating asthma (particularly
CC allergic asthma) or other respiratory problems (e.g. anaphylaxis,
CC hypersensitivity to an antigenic molecule or blood group
CC incompatibility), to treat and/or prevent organ rejection or graft-versus
CC host disease (GVHD), to modulate inflammation (septic shock, sepsis,
CC arthritis, nephritis, cytokine or chemokine induced lung injury,
CC inflammatory bowel disease, Crohn's disease, or resulting from over
CC production of cytokines), to treat hyperproliferative disorders,
CC including neoplasms in the abdomen, bone, breast, digestive system,
CC liver, pancreas, peritoneum, endocrine glands, eye, head and neck, soft
CC nervous (central and peripheral), lymphatic system, pelvic, skin, soft
CC tissue, spleen, thoracic and urogenital, hypergammaglobulinemia,
CC lymphoproliferative disorders, Waldenstrom's macroglobulinemia,
CC sarcoidosis), to treat or detect infectious agents, e.g. viruses (e.g.
CC arthritis, bronchiolitis, encephalitis, eye infections, chronic fatigue
CC syndrome, hepatitis, meningitis, AIDS, pneumonia, chickenpox, measles,
CC mumps, parainfluenza, rabies, the common cold, polio, leukemia, rubella,
CC sexually transmitted diseases, or skin diseases) bacterial or fungal
CC agents (e.g. bacteremia, endocarditis, eye infections, gingivitis,
CC opportunistic infections, respiratory tract infections, Lyme disease,
CC cat-scratch disease, paratyphoid fever, food poisoning, pneumonia,
CC gonorrhea and sexually transmitted diseases, meningitis, tuberculosis,
CC lupus, gangrene, tetanus, rheumatic fever, urinary tract infections,
CC wound infections), parasitic agents (e.g. scabies, dysentery, liver
CC disease, malaria, toxoplasmosis), to differentiate, proliferate and
CC attract cells, leading to the regeneration of tissues (e.g. repair,
CC replace or protect tissue in wounds, burns, incisions or ulcers,
CC osteoporosis, osteoarthritis, periodontal disease, liver failure,
CC surgery, cosmetic plastic surgery, reperfusion injury) to proliferate and
CC differentiate nerve cells (e.g. spinal cord disorders, head trauma,
CC cerebrovascular disease and stroke), localized neuropathies and central
CC nervous system diseases (e.g. Alzheimer's disease, Parkinson's disease,
CC Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager
CC syndrome). They may also increase or decrease the differentiation or
CC proliferation of embryonic stem cells and hematopoietic lineage, may be
CC used to modulate mammalian characteristics such as body height, weight,
CC hair color, eye color, skin, percentage of adipose tissue, pigmentation,
CC size, and shape, to modulate mammalian metabolism affecting catabolism,
CC anabolism, processing, utilization and storage of energy, to change a
CC mammal's mental state or physical state by influencing biohythms,
CC cardiac rhythms, circadian rhythms, depression (including depressive
CC disorders), tendency for violence, tolerance for pain, reproductive
CC capabilities, hormonal or endocrine levels, appetite, libido, memory,
CC stress, or other cognitive qualities, as a food additive or preservative,
CC such as to increase or decrease storage capabilities, fat content, lipid,
CC protein, carbohydrate, vitamins, minerals, cofactors or other nutritional
CC components. Mutations in the PNs or the presence or amount of expression
CC or activity of the polypeptides can be used for diagnosing a pathological

CC condition or a susceptibility to a pathological condition. The CTGF-4
CC polypeptides can also be used for identifying binding partners. The
CC products can also be used for producing transgenic animals. The present
CC sequence represents the CTGF-4 encoding cDNA.
XX
SQ Sequence 3658 BP; 984 A; 851 C; 841 G; 982 T; 0 other;

Query Match 100.0%; Score 3658; DB 21; Length 3658;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cggacttaccacagctccacagctgagacacccctccacagcccccattctgaagtgc 60
DB 1 cggacttaccacagctccacagctgagacacccctccacagcccccattctgaagtgc 60
OY 61 catgtatgagccgcatccaccccgctgcccgttgggggagcccatatcagatg 120
DB 61 catgtatgagccgcatccaccccgctgcccgttgggggagcccatatcagatg 120
OY 121 gctgtatgctgtatgagctgtgctcagagcttgaggacactgacagagctgcga 180
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OY 601 tgggt 660
DB 601 tgggt 660
OY 661 ggccttcgacactgt 720
DB 661 ggccttcgacactgt 720
OY 721 agtgcctgt 780
DB 721 agtgcctgt 780
OY 781 ggcacagcctctctac 840
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OY 841 cctacaagcttaagactatcagactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 900
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QY 2041 ttgtagcagccctggggttaacctctgagctggaagctgttggaactccaggggccccgt 2100
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QY 2101 gtccaagacacatctatccaagactatccaagcctctctgctctgagcacaatg 2160
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QY 2521 tcaagatcgaatattggaactgcttcttaaacacacatttcccccgttttagagctcca 2580
Db 2521 tcaagatcgaatattggaactgcttcttaaacacacatttcccccgttttagagctcca 2580
QY 2581 aatgtgtcagaataagaaacacatgtaataatgagcttgatttttaattcaatttcc 2640
Db 2581 aatgtgtcagaataagaaacacatgtaataatgagcttgatttttaattcaatttcc 2640
QY 2641 ctcttaagctcttctcagcctcttccaaagacggaatctgtaatttctgataatt 2700
Db 2641 ctcttaagctcttctcagcctcttccaaagacggaatctgtaatttctgataatt 2700
QY 2701 aggtgttaagcattccaaataatagtgagacacaaataccaggaatcccccgtgagct 2760
Db 2701 aggtgttaagcattccaaataatagtgagacacaaataccaggaatcccccgtgagct 2760
QY 2761 attccctcttcccatcggaacacagctctcaatcaacatttaagaatgattctgttac 2820
Db 2761 attccctcttcccatcggaacacagctctcaatcaacatttaagaatgattctgttac 2820
QY 2821 ccaatgctgataatgaattgtgtgagatattcaagaggaatctgtgagagtgacaga 2880
Db 2821 ccaatgctgataatgaattgtgtgagatattcaagaggaatctgtgagagtgacaga 2880
QY 2881 gaattctcaaaagggaaagagctggaataacatctcctactgtgacctcccaaaa 2940
Db 2881 gaattctcaaaagggaaagagctggaataacatctcctactgtgacctcccaaaa 2940
QY 2941 cctagtcagtggaaggtatcacagtgtgtctcaatcaatcttgatgaatacagaagct 3000
Db 2941 cctagtcagtggaaggtatcacagtgtgtctcaatcaatcttgatgaatacagaagct 3000
QY 3001 gtgcaagtttctctactttatctcgaagcctcttctccaaagcctacagaataatagaa 3060
Db 3001 gtgcaagtttctctactttatctcgaagcctcttctccaaagcctacagaataatagaa 3060
QY 3061 tttaacagtcacaaatttataatagtgcttagaagaaagagacattataattccaaa 3120
Db 3061 tttaacagtcacaaatttataatagtgcttagaagaaagagacattataattccaaa 3120

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OY 3121 gaaatgcatactgatacacaataatttgatagcgtatgcagaagattctgtatataa 3180
    |||||||
DB 3121 gaaatgcatactgatacacaataatttgatagcgtatgcagaagattctgtatataa 3180
OY 3181 gagaattcactccatgataatgtatctctctgttaagtcagttgaaatctgtatattct 3240
    |||||||
DB 3181 gagaattcactccatgataatgtatctctctgttaagtcagttgaaatctgtatattct 3240
OY 3241 gagaatgaaacacccctgcctctcaataattacaagctgtgataacagctcaatccattg 3300
    |||||||
DB 3241 gagaatgaaacacccctgcctctcaataattacaagctgtgataacagctcaatccattg 3300
OY 3301 aaattcctgtgaaacacccagagctaggttcttactgtaatttgatcctcaatttgggaaac 3360
    |||||||
DB 3301 aaattcctgtgaaacacccagagctaggttcttactgtaatttgatcctcaatttgggaaac 3360
OY 3361 tgaacttaagcttcaaaagatcatatgaaatcgtgttgagaactaggaattatctggc 3420
    |||||||
DB 3361 tgaacttaagcttcaaaagatcatatgaaatcgtgttgagaactaggaattatctggc 3420
OY 3421 aaatgggtggaggaaggtggtcagataacacccagctgcagctgttggagaacaggaact 3480
    |||||||
DB 3421 aaatgggtggaggaaggtggtcagataacacccagctgcagctgttggagaacaggaact 3480
OY 3481 attctatgcagagcccgagggcgaagtcacacccatgggttgagaacaggaagga 3540
    |||||||
DB 3481 attctatgcagagcccgagggcgaagtcacacccatgggttgagaacaggaagga 3540
OY 3541 aaattgatacccaatgataatgaagctcttcttaagtcagaatttccctgcgaattgtggc 3600
    |||||||
DB 3541 aaattgatacccaatgataatgaagctcttcttaagtcagaatttccctgcgaattgtggc 3600
OY 3601 ctgattcaataaataatcaagataataataatgtaaaataaataaataaataaataaataa 3658
    |||||||
DB 3601 ctgattcaataaataatcaagataataataatgtaaaataaataaataaataaataaataa 3658

RESULT 2
X76482
ID X76482 standard: DNA; 2830 BP.
XX
AC X76482:
XX
06-AUG-1999 (first entry)
XX
DE Human WISP-1 protein nucleotide sequence SEQ ID NO:1.
XX
KW WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
KW connective tissue growth factor; cancer; melanoma; arteriosclerosis;
KW leukaemia; lymphoid malignancy; haematopoiesis-related disorder;
KW tissue growth disorder; skin disorder; desmoplasia; fibrotic lesion;
KW kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
KW connective tissue disorder; catabolic state; inflammation;
KW testicular-related disorder; angiogenesis; immunological disorder; ss.
XX
OS Homo sapiens.
XX
PN M09921998-A1.
XX
PD 06-MAY-1999.
XX
PF 29-OCT-1998; 98MO-US22991.
XX
PR 14-APR-1998; 98US-0081695.
PR 29-OCT-1997; 97US-0063704.
PR 03-FEB-1998; 98US-0073612.
XX
PA (GETH ) GENENTECH INC.
XX
PI Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;
PI Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;
XX

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DR WPI; 1999-337420/28.
DR P-PSDB; Y17641.
XX
PT New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3
XX
PS Example 3; Page 159-161; 284pp; English.
XX
The present invention describes Wnt-1 induced secreted polypeptides,
CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2
CC and WISP-3 have homology to connective tissue growth factor (CTGF).
CC Products from the present invention can be used to treat WISP-related
CC disorders such as breast, ovarian, and colon cancer or melanoma. The
CC products can be used to treat arteriosclerosis. The products can also be
CC used to treat other diseases e.g. benign and malignant tumours,
CC leukaemia and lymphoid malignancies, neuronal, glial, astrocytal,
CC hypohalamic and other glandular, macropapal, epithelial, stromal, and
CC blastocellic disorders, haematopoiesis-related disorders, tissue-growth
CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney
CC disorders, bone-related disorders such as osteoporosis, trauma such as
CC burns, incisions, and other wounds, connective tissue disorders,
CC catabolic states, testicular-related disorders, and inflammatory,
CC angiogenic and immunologic disorders including arteriosclerosis. The
CC products can also be used for detection and diagnosis especially of
CC individuals with neoplastic cell growth or proliferation. The products
CC can be used in the production of transgenic or knock-out animals.
CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
CC cells.
XX
SO Sequence 2830 BP; 690 A; 736 C; 696 G; 708 T; 0 other;

Query Match 71.4%; Score 2611.8; DB 20; Length 2830;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2624; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 2 ggaattaccccaagctccactggaagacactctcaccgcccattctgcgaagggc 61
    |||||||
DB 184 ggaattaccccaagctccactggaagacactctcaccgcccattctgcgaagggc 243
OY 62 atgtgaatgcccgcacatcccccaccccgctgcgggtgagctcatcacaatgg 121
    |||||||
DB 244 atgtgaatgcccgcacatcccccaccccgctgcgggtgagctcatcacaatgg 303
OY 122 ctgtgaatgctgaatgctgctcagcagctctggggaacatgcaggaagctggcat 181
    |||||||
DB 304 ctgtgaatgctgaatgctgctcagcagctctggggaacatgcaggaagctggcat 363
OY 182 ctgtgaaccccaacggggtctctactgtgaatcagcgggagccggcgtaagcaat 241
    |||||||
DB 364 ctgtgaaccccaacggggtctctactgtgaatcagcgggagccggcgtaagcaat 423
OY 242 aggaatgtgtgcacaggtgtgctggtggtcgtcctctgtaatgggtgtgcacaaca 301
    |||||||
DB 424 aggaatgtgtgcacaggtgtgctggtggtcgtcctctgtaatgggtgtgcacaaca 483
OY 302 cggccaaatctcccaagctcaactgcagagtaacaactgcagctgcagcgcggtggg 361
    |||||||
DB 484 cggccaaatctcccaagctcaactgcagagtaacaactgcagctgcagcgcggtggg 543
OY 362 ctgcacacacacatgtgctcctcgaatgcgcccgcggtctgtgtgccccaacggcgcg 421
    |||||||
DB 544 ctgcacacacacatgtgctcctcgaatgcgcccgcggtctgtgtgccccaacggcgcg 603
OY 422 cgtgaagatactgtgacactgctgtgacgtgtgtaatgtgagaagacgacgaagggc 481
    |||||||
DB 604 cgtgaagatactgtgacactgctgtgacgtgtgtaatgtgagaagacgacgaagggc 663
OY 482 acgcaagaacgacaccccggtacacagagacgtctgataatgtgtgaggttgaggagatg 541
    |||||||
DB 664 acgcaagaacgacaccccggtacacagagacgtctgataatgtgtgaggttgaggagatg 723
OY 542 gcaacgaactgcatagctacacaagccctggagccttgcctcaacagctggcgct 601
    |||||||

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QY	1662	aaatttgaataaacctcttccttcttgaatgaggaaagcccccaagttaataatccagaagcagg	174.1
Db	1664	aaattctgataaacctctccctctgtatgaggaaagccccccagtttaatactccagaagcagg	192.23
QY	1742	aaaggtcaagccattctcaagaagaaaccaattgactctcaacatgaaatcagctgtcagtcag	180.1
Db	1924	aaaggtcaagccattctcaagaagaaaccaattgactctcaacatgaaatcagctgtcagtcag	198.3
QY	1802	cagggtcttgaggcaatttgccagagctctctcccttgaaatctctccctgtctcgtctgggg	186.1
Db	1984	cagggtcttgaggcaatttgccagagctctctcccttgaaatctctccctgtctcgtctt..999	204.2
QY	1862	ttcttaagaatttggtaagggcctcttgagacgtgcctgtctctggccccctggagagtggtccct	192.1
Db	2043	ttcttaagaatttggtaagggcctcttgagacgtgcctgtctctggccccctggagagtggtccct	210.2
QY	1932	gaacaacccctctaactctctcaagaagcctctgagagaccacagctgcagacatgacgaacca	198.1
Db	2103	gaacaacccctctaactctctcaagaagcctctgagagaccacagctgcagacatgacgaacca	216.5
QY	1982	ctgaaatgacccaagaacaggtctcaggtgaagggtgtgtgggtcaaaacccaagaagtggtgtccct	204.1
Db	2163	ctgaaatgacccaagaacaggtctcaggtgaagggtgtgtgggtcaaaacccaagaagtggtgtccct	222.2
QY	2042	tgtgtgaagagcctgggtgtgacacctcttaagagctgtggaggtgtgtgggaactccagggccccctg	210.1
Db	2223	tgtgtgaagagcctgggtgtgacacctcttaagagctgtggaggtgtgtgggaactccagggccccctg	228.3
QY	2102	ttcagagacacatcatctctgcagagaaatcaattctcaacagccttctgtctgtcagcaaatg	216.1
Db	2283	ttcagagacacatcatctctgcagagaaatcaattctcaacagccttctgtctgtcagcaaatg	234.4
QY	2162	ccagttctctgtgtgaggaagatggaaggttaccaggtgtgttagaagaacagaagaatagacttaa	222.1
Db	2343	ccagttctctgtgtgaggaagatggaaggttaccaggtgtgttagaagaagaagaatagacttaa	240.2
QY	2222	taaaaggttttaaaagttgaaggggtttgaagccttaaaaggaagaaggttgtgtgttaatgtaatac	228.1
Db	2403	taaaaggttttaaaagttgaaggggtttgaagccttaaaaggaagaaggttgtgtgttaatgtaatac	246.5
QY	2282	aggcatatattatctgtatctaggaagaaataataattactgtatagaaattctttattag	234.1
Db	2463	aggcatatattatctgtatctaggaagaaataataattactgtatagaaattctttattag	252.2
QY	2342	ggcctttctctgtccagagacatgtcctcagtgcttgaagttaatgactcactgaactct	240.1
Db	2523	ggcctttctctgtccagagacatgtcctcagtgcttgaagttaatgactcactgaactct	258.3
QY	2402	cagagacaattgttggagaaggttcccatattatattctctttcttcaaaatgagaaagggaagc	246.1
Db	2583	cagagacaattgttggagaaggttcccatattatattctctttcttcaaaatgagaaagggaagc	264.4
QY	2462	tcatagaggttgaagaaacatcaacacagatgacccagtttgtagcttgagggaagttaggtt	252.1
Db	2643	tcatagaggttgaagaaacatcaacacagatgacccagtttgtagcttgagggaagttaggtt	270.2
QY	2522	cagatcgaaatttgactgtctttataaacacatatcttcccccgtgttttagagcttccaa	258.1
Db	2703	cagatcgaaatttgactgtctttataaacacatatcttcccccgtgttttagagcttccaa	276.3
QY	2582	atgtgtcaggaattaggaagaacatgacgaataaataagctgtgatttttaa 2628	
Db	2763	atgtgtcaggaattaggaagaacatgacgaataaataagctgtgatttttttaa 2809	
RESULT 3			
X76490			
ID	X76490 standard: DNA; 1403 BP.		
XX			
KC	X76490.		
DT	06-AUG-1999 (first entry)		

RESULT	3	
X76490		
ID	X76490	standard; DNA; 1403 BP
XX		
AC	X76490;	
XX		
DT	06-AUG-1999	(first entry)

```

XX Human WISP-1 clone 568.13.
XX
XX MN-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
XX connective tissue growth factor; cancer; melanoma; arteriosclerosis;
XX leukemia; lymphoid malignancy; hematopoiesis-related disorder;
XX tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
XX kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
XX connective tissue disorder; catabolic state; inflammation;
XX testicular-related disorder; angiogenesis; immunological disorder; ss.
XX
XX Homo sapiens.
XX
XX PN MO9921998-AI.
XX
XX PD 06-MAY-1999.
XX
XX PF 29-OCT-1998; 98WO-US22991.
XX
XX PR 14-APR-1998; 98US-0081695.
XX PR 29-OCT-1997; 97US-0063704.
XX PR 03-FEB-1998; 98US-0073612.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;
XX Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;
XX MPI, 1999-337420/28.
XX
XX PT New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3
XX PS Clalm 8; Page 184-185; 284pp; English.
XX
XX CC The present invention describes Wnt-1 induced secreted polypeptides,
XX CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2
XX CC and WISP-3 have homology to connective tissue growth factor (CTGF).
XX CC Products from the present invention can be used to treat WISP-related
XX CC disorders such as breast, ovarian, and colon cancer or melanoma. The
XX CC products can be used to treat arteriosclerosis. The products can also be
XX CC used to treat other diseases e.g. benign and malignant tumours,
XX CC leukemia and lymphoid malignancies, neuronal, glial, astrocytal,
XX CC hypothalamic and other glandular, macrophagel, epithelial, stromal, and
XX CC blastocoelel disorders, hematopoiesis-related disorders, tissue-growth
XX CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney
XX CC disorders, bone-related disorders such as osteoporosis, trauma such as
XX CC burns, incisions, and other wounds, connective tissue disorders,
XX CC catabolic states, testicular-related disorders, and inflammatory'. The
XX CC angiogenic and immunologic disorders including arteriosclerosis. The
XX CC products can also be used for detection and diagnosis especially of
XX CC individuals with neoplastic cell growth or proliferation. The products
XX CC can be used in the production of transgenic or knock-out animals.
XX CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
XX CC cells.
XX
XX SQ Sequence 1403 BP; 277 A; 446 C; 378 G; 302 T; 0 other:

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[illegible]

RESULT 4
X76483/C
ID X76483 standard: DNA; 1101 BP.
XX
XX X76483;
XX
XX 06-AUG-1999 (first entry)
XX
XX Human WISP-1 protein complementary nucleotide sequence SEQ ID NO:2.
XX
XX WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
XX connective tissue growth factor; cancer; melanoma; arteriosclerosis;
XX leukemia; lymphoid malignancy; haematopoiesis-related disorder;
XX tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
XX kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
XX connective tissue disorder; catabolic state; inflammation;
XX testicular-related disorder; angiogenesis; immunological disorder; ss.
XX
XX Homo sapiens.
XX
XX MO9921998-A1.
XX
XX 06-MAY-1999.
XX
XX 29-OCT-1998; 98MO-US22991.
XX
XX 14-APR-1998; 98US-0081695.
XX 29-OCT-1997; 97US-0063704.
XX 03-FEB-1998; 98US-0073612.
XX
XX (GETH) GENENTECH INC.
XX
XX Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;
XX Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;
XX
XX WPI; 1999-337420/28.
XX
XX New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3
XX
XX
XX Disclosure; Page 161-162; 284pp; English.
XX
XX The present invention describes Wnt-1 induced secreted polypeptides,
XX WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2
XX and WISP-3 have homology to connective tissue growth factor (CTGF).
XX Products from the present invention can be used to treat WISP-related
XX disorders such as breast, ovarian, and colon cancer or melanoma. The
XX products can be used to treat arteriosclerosis. The products can also be
XX used to treat other diseases e.g. benign and malignant tumours,
XX leukemia and lymphoid malignancies, neuronal, glial, astrocytal,
XX hypochromic and other glandular, macrophagal, epithelial, stromal, and
XX blastocoele disorders, haematopoiesis-related disorders, tissue-growth
XX disorders, skin disorders, desmoplasia, fibrotic lesions, kidney
XX disorders, bone-related disorders such as osteoporosis, trauma such as
XX burns, incisions, and other wounds, connective tissue disorders,
XX catabolic states, testicular-related disorders, and inflammatory,
XX angiogenic and immunologic disorders including arteriosclerosis. The
XX products can also be used for detection and diagnosis especially of
XX individuals with neoplastic cell growth or proliferation. The products
XX can be used in the production of transgenic or knock-out animals.
XX Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
XX cells.
XX
XX Sequence 1101 BP; 219 A; 310 C; 354 G; 218 T; 0 other;
XX
XX

Query Match 27.5%; Score 1004.4; DB 20; Length 1101;
Best Local Similarity 99.9%; Prod. NO. 5e-245;
Matches 1005; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 2 ggaattacccagctcagctgagagacacccctcagcccaatctgcaagtgacc 61
1006 ggaattacccagctcagctgagagacacccctcagcccaatctgcaagtgacc 61
1006 ggaattacccagctcagctgagagacacccctcagcccaatctgcaagtgacc 61

62 atgtgagtgccgcagcatcccccacccgcctgcccctgggggtcagcctcaccagatgg 121
946 atgtgagtgccgcagcatcccccacccgcctgcccctgggggtcagcctcaccagatgg 887
122 ctgtgagtgctgtgaagatgtgcctcagcagccttggggagacatgcaaggagctgcat 181
886 ctgtgagtgctgtgaagatgtgcctcagcagccttggggagacatgcaaggagctgcat 827
182 ctgtgagtgctgtgaagatgtgcctcagcagccttggggagacatgcaaggagctgcat 241
826 ctgtgagtgctgtgaagatgtgcctcagcagccttggggagacatgcaaggagctgcat 767
242 aggaagtgtgtgcaagatgt 301
766 aggaagtgtgtgcaagatgt 707
302 cggcagctccctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 361
706 cggcagctccctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 647
362 ctgtgagtgctgtgaagatgtgcctcagcagccttggggagacatgcaaggagctgcat 421
646 ctgtgagtgctgtgaagatgtgcctcagcagccttggggagacatgcaaggagctgcat 587
422 cgtgagatatacctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 481
586 cgtgagatatacctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 527
482 acgcaagaccgaccccccgtgtacacagagacccctcagcagccttggggagacatgca 541
526 acgcaagaccgaccccccgtgtacacagagacccctcagcagccttggggagacatgca 467
542 gcaagagacatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 601
466 gcaagagacatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcatgcat 407
602 gggggtctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 661
406 gggggtctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 347
662 cctctgcaactctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 721
346 cctctgcaactctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 287
722 gttctgt 781
286 gttctgt 227
782 caaacgctcctac 841
226 caaacgctcctac 167
842 ctacaagctcctac 901
166 ctacaagctcctac 107
902 ccaggtctcctac 961
106 ccaggtctcctac 47
962 cttgt 1007
46 cttgt 1

RESULT 5
X76484
ID X76484 standard: DNA; 1766 BP.
XX
XX X76484;
XX
XX 06-AUG-1999 (first entry)
XX

XX Mouse WISP-1 protein nucleotide sequence SEQ ID NO:9.
 DE
 XX
 XX WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;
 KM connective tissue growth factor; cancer; melanoma; arteriosclerosis;
 KM leukemias; lymphoid malignancy; haematopoiesis-related disorder;
 KM tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;
 KM kidney disorder; bone-related disorder; osteoporosis; trauma; burn;
 KM connective tissue disorder; cataplastic state; inflammation;
 KM testicular-related disorder; angiogenesis; immunological disorder; ss.
 OS
 XX Mus sp.
 XX
 XX W09921998-A1.
 XX
 XX 06-MAY-1999.
 XX
 XX 29-OCT-1998; 98MO-US22991.
 XX
 XX 14-APR-1998; 98US-0081695.
 XX 29-OCT-1997; 97US-0063704.
 XX 03-FEB-1998; 98US-0073612.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Botstein DA, Cohen RU, Goddard A, Gurney AL, Hillan K;
 PI Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;
 XX
 XX PFI: 1999-337420/28.
 XX P-PSDB; Y17647.
 DR
 XX
 XX New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3
 PT
 XX
 XX Example 1: Page 170-171; 284pp; English.
 PS
 XX
 XX The present invention describes Wnt-1 induced secreted polypeptides,
 CC WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2
 CC and WISP-3 have homology to connective tissue growth factor (CTGF).
 CC Products from the present invention can be used to treat WISP-related
 CC disorders such as breast, ovarian, and colon cancer or melanoma. The
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 CC leukemia and lymphoid malignancies, neuronal, glial, astrocytal,
 CC hypochalamic and other glandular, macrophagal, epithelial, stromal, and
 CC blastocoeic disorders, hematopolesis-related disorders, tissue-growth
 CC disorders, skin disorders, desmoplasia, fibrotic lesions, kidney
 CC disorders, bone-related disorders such as osteoporosis, trauma such as
 CC burns, incisions, and other wounds, connective tissue disorders,
 CC cataplastic states, testicular-related disorders, and inflammatory,
 CC angiogenic and immunologic disorders including arteriosclerosis. The
 CC products can also be used for detection and diagnosis especially of
 CC individuals with neoplastic cell growth or proliferation. The products
 CC can be used in the production of transgenic or knock-out animals.
 CC Antibodies can be used to induce death in WISP-1, 2 or 3 overexpressing
 CC cells.
 CC
 XX
 XX Sequence 1766 BP; 406 A; 497 C; 460 G; 402 T; 1 other;
 SQ

Query Match 22.3%; Score 815.4; DB 20; Length 1766;
 Best Local Similarity 71.9%; Pred. No. 5.5e-197;
 Matches 1133; Conservative 0; Mismatches 436; Indels 8; Gaps 5;
 QY 5 cttaaccagctccatctgagacacccctccacgcccccaattctgcaagtgcacatg 64
 DB 177 cttaaccagctccatctgagacacccctccacgcccccaattctgcaagtgcacatg 236
 QY 65 tgaatgcgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 124
 DB 237 tgaatgcgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 296
 QY 125 tgaatgcgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 184
 DB 297 tgaatgcgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 356
 QY 185 tgaatgcgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 244
 DB 357 tgaatgcgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 416
 QY 245 agtgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 304
 DB 417 agtgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 476
 QY 305 ccaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 364
 DB 477 ccaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 536
 QY 365 ccaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 424
 DB 537 ccaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 596
 QY 425 gagaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 484
 DB 597 gagaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 656
 QY 485 ccaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 544
 DB 657 ccaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 716
 QY 545 ccaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 604
 DB 717 ccaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 776
 QY 605 ggcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 664
 DB 777 ggcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 836
 QY 665 cgcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 724
 DB 837 cgcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 896
 QY 725 tgcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 784
 DB 897 tgcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 956
 QY 785 agcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 844
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 QY 845 cagctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 904
 DB 1017 cagctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 1076
 QY 905 ggcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 964
 DB 1077 ggcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 1136
 QY 965 tgcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 1024
 DB 1137 tgcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 1196
 QY 1025 tgcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 1084
 DB 1197 tgcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 1256
 QY 1085 tgcctgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 1142
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 QY 1203 tcaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 1262
 DB 1376 tcaatgcctgcgcacatcccaacccgcctgcgcgcgtgaggtcagcctcatcacagatgctg 1435

Oy	1263	gctcgatcccaagcctttccaaagtcacagtagaagtcctgctgtagcttgcct---aaatccca	1319
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Oy	1320	agaaatgtaacacagtagagacttttaatacatcaactaattctctcttagatgccaaaccaca	1379
Db	1496	aggaagaagcaccagctcgtagaagaccagatcatctgagtcctctccatgagtcagaagcc-ta	1554
Oy	1380	agactctttgggtccatctcagaatgaatagatggaatttggaaacaataagaatactatcta	1439
Db	1555	gggagctcgagatccctcttcacagacagatgtagatggatgggacacagaataagcatatta	1614
Oy	1440	tttggagcctcccaagagtagtacttaattggttaatttgcg-ctcagcgacacaaacta	1498
Db	1615	tttaaccttgcacaaatgatactatccctgggattcttcgtcctaanaacatacaaaagtg	1674
Oy	1499	tcctgattccaataatgatatgacacctcaagtcacatcaaacatttgcacagtgagttgaat	1558
Db	1675	ttcttgctccactgactcgtatcatcacaagaatcacacaacatttccagctgaggaacctat	1734
Oy	1559	agttgcttaatttggattt	1577
Db	1735	agttgtgcatctcgtttt	1753
RESULT	6		
ID	X/76493		
AC	X/76493 standard; DNA; 1202 BP.		
XX	X/76493;		
DT	06-AUG-1999 (first entry)		
DE	Human WISP-1 clone 568.4A.		
XX			
XX	Wnt-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;		
KW	connective tissue growth factor; cancer; melanoma; arteriosclerosis;		
KM	leukaemia; lymphoid malignancy; haematopoiesis-related disorder;		
KM	tissue growth disorder; skin disorder; desmoplasia; fibrotic lesion;		
KM	kidney disorder; bone-related disorder; osteoporosis; trauma; burn;		
KW	connective tissue disorder; catabolic state; inflammation;		
XX	testicular-related disorder; angiogenesis; immunological disorder; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W09921998-A1.		
XX			
PD	06-MAY-1999.		
XX			
PE	29-OCT-1998; 98WO-US22991.		
XX			
PR	14-APR-1998; 98US-0081695.		
PR	29-OCT-1997; 97US-0063704.		
PR	03-FEB-1998; 98US-0073612.		
XX			
PA	(GETH) GENENTECH INC.		
PI	Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;		
PI	Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;		
XX			
DR	WPI; 1999-337420/28.		
XX			
PT	New isolated wnt-1 induced secreted polypeptides, WISP-1, 2 and 3		
PS	Claim 8; Page 186-187; 284pp; English.		
CC	The present invention describes Wnt-1 induced secreted polypeptides,		
CC	WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP-2		
CC	and WISP-3 have homology to connective tissue growth factor (CTGF).		
CC	Products from the present invention can be used to treat WISP-related		
CC	disorders such as breast, ovarian, and colon cancer or melanoma. The		
CC	products can be used to treat arteriosclerosis. The products can also be		

[illegible]

Db	143	atgcttgagggtgagtgatggtccacaggaaactgcataagcctatacacaagcccttga	202
Qy	577	gacctgctccaccagctcgcgccttgggggtctccactcggatctccaatgttaacgcc	636
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Qy	637	agttcttgccctggacgaagagagccgcctctgcgaacttggcgcatgcatgtggacatcc	696
Db	263	agttcttgccctggacgaagagagccgcctctgcgaacttggcgcatgcatgtggacatcc	322
Qy	697	atacacatcaaaagccagggaaagaagtgtctgtgctgtgtaccagccagggcgatccatga	756
Db	323	atacacatcaaaagccagggaaagaagtgtctgtgctgtgtaccagccagggcgatccatga	382
Qy	757	acttacacttgcgggctgcataagaacacgcctctcatcaacccaagtcttggagttt	816
Db	383	acttacacttgcgggctgcataagaacacgcctctcatcaacccaagtcttggagttt	442
Qy	817	gcataggcaataagtgctgtcatctccctacaagaactaagactatcgacgctctccagtt	876
Db	443	gcataggcaataagtgctgtcatctccctacaagaactaagactatcgacgctctccagtt	502
Qy	877	gtctcgtaggcttgcttcccgccaggtctcctatgattat	920
Db	503	gtctcgtaggcttgcttcccgccaggtctcctatgattat	546
RESULT	11		
ID	X76492		
XX	X76492 standard; DNA; 683 BP.		
XX	X76492;		
XX	06-AUG-1999 (first entry)		
XX	Human WISP-1 clone 568.39.		
XX	WNT-1 induced secreted protein; WISP-1; WISP-2; WISP-3; CTGF; tumour;		
XX	connective tissue growth factor; cancer; melanoma; arteriosclerosis;		
XX	leukemia; lymphoid malignancy; haematopoiesis-related disorder;		
XX	tissue-growth disorder; skin disorder; desmoplasia; fibrotic lesion;		
XX	kidney disorder; bone-related disorder; osteoporosis; trauma; burn;		
XX	connective tissue disorder; catabolic state; inflammation;		
XX	testicular-related disorder; angiogenesis; immunological disorder; ss		
XX	Homo sapiens.		
XX	OS		
XX	PN		
XX	W09921998-A1.		
XX	06-MAY-1999.		
XX	29-OCT-1998; 98WO-US22921.		
XX	14-APR-1998; 98US-0081695.		
XX	29-OCT-1997; 97US-0063704.		
XX	03-FEB-1998; 98US-0073612.		
PA	(GETH) GENENTECH INC.		
FI	Botstein DA, Cohen RL, Goddard A, Gurney AL, Hillan K;		
FI	Lawrence DA, Levine AJ, Pennica D, Roy MA, Wood WI;		
XX	WPI; 1999-337420/28.		
XX	New isolated Wnt-1 induced secreted polypeptides, WISP-1, 2 and 3		
XX	Claim 8; Page 186; 284pp; English.		
XX	The present invention describes Wnt-1 induced secreted polypeptides,		
XX	WISP-1, 2 and 3. The novel WISP polypeptides, designated WISP-1, WISP		
XX	and WISP-3 have homology to connective tissue growth factor (CTGF).		
XX	Products from the present invention can be used to treat WISP-related		

Query Match	11.0%	Score 403.4	DB 20	Length 683
Best Local Similarity	99.8%	Pred. No. 1e-92		
Matches 404	Conservative	0	Mismatches 2	Indels 1
			Gaps 0	
QY 516 gatgctgtggtggaagttaggcatacggcccaagaactgatatagccatacacaagcccttg	575			
DB 279 gatgctgtggtggaagttaggcatacggcccaagaactgatatagccatacacaagcccttg	338			
QY 576 agcccttgctccacacgacgctgcgctggtggtgtcctcactcggatccatgtttaaagcc	635			
DB 339 agcccttgctccacacgacgctgcgctggtggtgtcctcactcggatccatgtttaaagcc	398			
QY 636 cagtgctgctcgaagcaagaagacgcgcctctgcaacttgcggccatgctgagacac	695			
DB 399 cagtgctgctcgaagcaagaagacgcgcctctgcaacttgcggccatgctgagacac	458			
QY 696 cctaacactataaaggcaggaagaagtgtctgctgtgtacacgcaagaagcatctcag	755			
DB 459 cctaacactataaaggcaggaagaagtgtctgctgtgtacacgcaagaagcatctcag	518			
QY 756 aacttcacacttcggcgctgcatacgaacgctcctacaaaccccaagctcgtgagtt	815			
DB 519 aacttcacacttcggcgctgcatacgaacgctcctacaaaccccaagctcgtgagtt	578			
QY 816 tgcattggaacaataggctgctgcatacctccctacaagtctaaagactatcgacgtgtccttcag	875			
DB 579 tgcattggaacaataggctgctgcatacctccctacaagtctaaagactatcgacgtgtccttcag	638			
QY 876 tgtctctgattggtctggtcttcctccgcagagctcctatgataat	920			
DB 639 tgtctctgattggtctggtcttcctccgcagagctcctatgataat	683			

RESULT 12

ID 258614 standard; CDNA; 540 BP.

AC 258614;

DT 11-APR-2000 (first entry)

DE Human, CTGF-4 related CDNA clone HSKXM68R.

KX Connective tissue growth factor-4; CTGF-4; human; immune system disorder; hematopoietic disorder; autoimmune disorder; diabetes mellitus; asthma; respiratory disorder; inflammation; hyperproliferative disorder; infection; central nervous system disease; Alzheimer's disease; AIDS; food additive; ss.

OS Homo sapiens

XX MO9962927-AL

QY 3640 aaaaaa 3647
 DB 15 AAAAAA 8

RESULT 14
 258616
 ID 258616 standard; CDNA; 311 BP.

AC 258616;
 XX
 XX
 DT 11-APR-2000 (first entry)
 XX
 XX
 DE Human CTGF-4 related CDNA clone HAPAO05R.

XX Connective tissue growth factor-4; CTGF-4; human; immune system disorder;
 KW hemopoietic disorder; autoimmune disorder; diabetes mellitus; asthma;
 KW respiratory disorder; inflammation; hyperproliferative disorder;
 KW infection; central nervous system disease; Alzheimer's disease; AIDS;
 KW food additive; ss.

XX Homo sapiens.
 OS
 XX
 PN MO9962927-A1.
 XX
 PD 09-DEC-1999.
 XX
 PF 03-JUN-1999; 99MO-US12150.
 XX
 PR 05-JUN-1998; 98US-0088320.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Young PE;
 XX
 DR WPI; 2000-147042/13.

PT New isolated connective tissue growth factor-4, used for treating e.g.
 XX cancers -
 PS
 XX
 XX Disclosure; Page 195; 196pp; English.

XX The invention provides an isolated human connective tissue growth factor
 CC -4 (CTGF-4) polypeptide. The CTGF-4 CDNA is deposited under ATCC No.
 CC 209816. The CTGF-4 protein can be expressed by standard recombinant
 CC methodology. The polypeptide can be used for preventing, treating or
 CC ameliorating a medical condition. (See 258613 for a detailed description
 CC of the diseases, deficiencies, disorders and infections that can be
 CC treated or prevented using the CTGF-4 polypeptide). Sequences 258614-619
 CC represent nucleotide sequences related to CTGF-4 CDNA.
 XX

XX Sequence 311 BP; 101 A; 54 C; 58 G; 96 T; 2 other;

Query Match 8.1%; Score 295.4; DB 21; Length 311;
 Best Local Similarity 98.7%; Pred. No. 1.7e-65;
 Matches 307; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 2833 attgaatgtgtgtagtattacacaggaattctgtgacgtgtgacagagattcctaa 2892
 DB 1 attgaatgtgtgtagtattacacaggaattctgtgacgtgtgacagagattcctaa 60
 QY 2893 cgggaaaaagactgggaatacattctctactgtgacctcccaaaacctagtcagtg 2952
 DB 61 cgggaaaaagactgggaatacattctctactgtgacctcccaaaacctagtcagtg 120
 QY 2953 caaggtatacagtggtgtctatttaatacttgatgaatacaggaagctgtgcatgttc 3012
 DB 121 caaggtatacagtggtgtctatttaatacttgatgaatacaggaagctgtgcatgttc 180
 QY 3013 ctactttatcgagagctctctctccaaagctacatgaanaagatttaacagta 3072

DB 181 ctactttnttcgaagctctctctccaaagctacatgaanaagatttaacagta 240
 QY 3073 aaatttatatagtgctcttagcaaaagagacattata-cttcaaaagatgcatat 3131
 DB 241 aaatttatatagtgctcttagcaaaagagacattata-cttcaaaagatgcatat 300
 QY 3132 gtagtatata 3142
 DB 301 gtagtatata 311

RESULT 15
 211246
 ID 211246 standard; DNA; 1062 BP.

AC 211246;
 XX
 XX
 DT 15-NOV-1999 (first entry)
 XX
 XX
 DE Human connective tissue growth factor, zctgf4, generic coding sequence.

XX Connective tissue growth factor; zctgf4; chromosome 6q abnormality;
 KW diagnosis; therapy; bone marrow fibrosis; haematopoietic cell production;
 KW haematopoietic cell differentiation; scar tissue formation; scleroderma;
 KW cutaneous lupus erythematosus; dermatosis; end-stage kidney failure;
 KW human; ss.

XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1062
 FT /*tag= a
 FT /product= zctgf4

XX MO9942583-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 19-FEB-1999; 99MO-US03585.
 XX
 PR 20-FEB-1998; 98US-0027405.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Jaspers SR, Sheppard PO;
 XX
 DR WPI; 1999-540308/45.
 DR P-PDSB; Y34190.

PT New isolated polynucleotides encoding connective tissue growth
 XX factor homologue polypeptides, used diagnostically
 PS
 XX
 XX Claim 5; Page 105; 122pp; English.

XX This sequence encodes the human connective tissue growth factor (zctgf4)
 CC of the invention. The zctgf4 coding sequence may be used to produce CTGF
 CC homologue polypeptides according to standard recombinant DNA
 CC methodologies. The zctgf4 DNAs may also be used diagnostically as probes
 CC to detect the presence of similar sequences in biological samples, and to
 CC identify abnormalities or mutations within those sequences. The sequences
 CC can be used to detect a chromosome 6q abnormality. Antagonists and
 CC antibodies of zctgf4 can be used to treat and diagnose bone marrow
 CC fibrosis, modulating production or differentiation of haematopoietic
 CC cells, prevention of scar tissue formation, cutaneous lupus
 CC erythematosus, scleroderma, dermatosis, and end-stage kidney failure.

XX Sequence 1062 BP; 291 A; 114 C; 175 G; 145 T; 437 other;

Query Match 7.6%; Score 277.8; DB 20; Length 1062;
 Best Local Similarity 38.7%; Pred. No. 9.2e-61;
 Matches 360; Conservative 179; Mismatches 400; Indels 24; Gaps 3;

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 07:14:19 ; Search time 1966.83 Seconds
(without alignments)
13032.845 Million cell updates/sec

Title: US-09-325-019-1
Perfect score: 3658
Sequence: 1 cgaacttaccacgcctcca.....aaaaaaaaaaaaaaaaaaaaa 3658

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 segs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

EST:*

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2:	gb_est2:*
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 180: em_estp79:*
 181: em_estp80:*
 182: em_estp81:*
 183: em_estp82:*
 184: em_estp83:*
 185: em_estp84:*
 186: em_estp85:*
 187: em_estp86:*
 188: em_estp87:*
 189: em_estp88:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	699	19.1	729	38	AV709609	AV709609 AV709609
2	565	15.4	565	23	AI917494	AI917494 t884f07.x
3	496.4	13.6	500	23	AI683855	AI683855 tx77h09.x
4	471	12.9	471	19	AI372923	AI372923 q299a05.x
5	461	12.6	469	22	AI624151	AI624151 t928e10.x
6	442.4	12.1	444	138	BE000447	BE000447 7h29b07.x
7	419.8	11.5	444	107	AI990199	AI990199 w838c03.x
8	415.4	11.4	417	107	BE350495	BE350495 h14f01.x
9	395	10.8	406	95	AW804917	AW804917 OVA-DM009
10	384.4	10.5	386	108	BE455934	BE455934 hy08a09.x
11	348.2	9.5	381	88	AW291772	AW291772 UT-H-B12
12	338.8	9.3	503	168	AQ726685	AQ726685 HS-5411-B
13	314.4	8.6	429	145	T55016	T55016 yd42e03.x
14	300	8.2	320	27	AI971546	AI971546 wq87b12.x
15	295.4	8.1	311	5	AA316760	AA316760 EST18843
16	292.2	8.0	297	13	AA922800	AA922800 om63h03.s
17	247	6.8	389	104	BE127024	BE127024 DEBA0773
18	234.4	6.4	606	38	AV670917	AV670917 AV670917
19	234	6.4	650	176	A2221725	A2221725 RPCI-23-9
20	208	5.7	208	20	AI473336	AI473336 t883f09.x
21	183.4	5.0	197	6	AA344487	AA344487 EST50540
22	181.2	4.9	562	22	AI588038	AI588038 mp02e12.y
23	178.2	4.9	562	22	AI588038	AI588038 mp02e12.y
24	161	4.4	161	6	AA393740	AA393740 zv64d08.x
25	135.2	3.7	1057	137	BE898435	BE898435 601681295
26	131	3.6	528	2	AA104304	AA104304 mp02e12.x
27	125	3.4	636	40	AW146261	AW146261 um39h01.x
28	124.4	3.4	1077	106	BE306545	BE306545 601102787
29	123	3.4	1077	192	CNS030FR	AI255888 Teltramdon
30	121.2	3.3	753	136	BE865071	BE865071 UT-M-BH2
31	118	3.2	578	37	AV600173	AV600173 AV600173
32	117.4	3.2	624	94	AW742404	AW742404 UP56f10.y
33	113.4	3.1	647	27	AI965085	AI965085 f886f04.y
34	113.4	3.1	680	38	AV702997	AV702997 AV702997
35	113	3.1	436	6	AA373233	AA373233 EST85240
36	113	3.1	843	191	CNS02CON	AI191408 Teltramdon
37	111.2	3.0	505	139	BE037009	BE037009 601456766
38	108.4	3.0	624	38	AV710966	AV710966 AV710966
39	107.4	2.9	696	4	AA221075	AA221075 mw75c04.x
40	107	2.9	475	9	AA605073	AA605073 no74d01.x
41	106.8	2.9	415	104	BE166172	BE166172 MR3-HT048
42	105.4	2.9	344	104	BE127370	BE127370 DEPA1119
43	105.4	2.9	531	7	AA419858	AA419858 w48b09.x
44	105.4	2.9	806	28	AL048446	AL048446 DKE25861
45	105.4	2.9	831	135	BE742330	BE742330 601575564

ALIGNMENTS

RESULT 1
 AV709609 AV709609 729 bp mRNA
 LOCUS AV709609 ABC Homo sapiens cDNA clone ADCAR05 5', mRNA sequence.
 DEFINITION AV709609
 ACCESSION AV709609
 VERSION AV709609.1 GI:10727426
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

QY 3076 ttattataatggtctcttcgcaaaagagacatttaatttcagaagaatgcatagtat 3135
 DB 565 ttttattattttagctcttgcacaaagacatttatttatttcaaaaatgacattatgtat 506
 QY 3136 gatacatatatttctgtatgctgcatgcaagaattctgtataaagaatttcacat 3195
 DB 505 gttatcatatttatttctgtatgctgcatgcaagaatttctgtataaagaatttcacat 446
 QY 3196 gaattgctctctctgtatgcaagtgatgcatgcatgtatgatttctgtagaagtgaaacacc 3255
 DB 445 gaattgctctctctgtatgcaagtgatgcatgcatgtatgatttctgtagaagtgaaacacc 386
 QY 3256 tgcacatctcaaatctcaaaagctggtgataacagctcctcattcttgaaattcagtgaaac 3315
 DB 385 tgcacatctcaaatctcaaaagctggtgataacagctcctcattcttgaaattcagtgaaac 326
 QY 3316 ccaaaagctgaggtctcttcacgaattcgcattcctcattcttgaaagcaactgacttca 3375
 DB 325 ccaaaagctgaggtctcttcacgaattcgcattcctcattcttgaaagcaactgacttca 266
 QY 3376 aagatcataggaagctctgttctggaagaactaggaattatcttgcaatggtggaaggaag 3435
 DB 265 aagatcataggaagctctgttctggaagaactaggaattatcttgcaatggtggaaggaag 206
 QY 3436 gtggtcagaataaccagctcagctcagctgttcttggaagaaggaactcttctgcaagcc 3495
 DB 205 gtggtcagaataaccagctcagctcagctgttcttggaagaaggaactcttctgcaagcc 146
 QY 3496 cgaagagcaagctcgaacccatggtggtggaagcagtggaagaattctgcaagcc 3555
 DB 145 cgaagagcaagctcgaacccatggtggtggaagcagtggaagaattctgcaagcc 86
 QY 3556 taattgaagctctcttcgaagtcgaattccctcgaagtggtggtcgaattcgaataaaa 3615
 DB 85 taattgaagctctcttcgaagtcgaattccctcgaagtggtggtcgaattcgaataaaa 26
 QY 3616 ttaagaataataataatgaa 3640
 DB 25 ttaagaataataataatgaa 1
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 LOCUS tx77h09.x1 NCI-CGAP_U11 Homo sapiens cDNA clone IMAGE:2275649 3,
 DEFINITION mRNA sequence.
 ACCESSION A1683855
 VERSION A1683855.1 GI:4894037
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNI at:
 www.bio.lnlni.gov/bdnp/image/image.html
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 High quality sequence stop: 403.
 Location/Qualifiers

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 /clone_lib="NCI CGAP_U11"
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 adenocarcinoma, 7 pooled tumors"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1; Salt;
 Site: 2; NCI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"
 BASE COUNT 158 a 91 c 101 g 150 t
 ORIGIN
 Query Match 13.6%; Score 496.4; DB 23; Length 500;
 Best Local Similarity 99.8%; Pred. No. 1.2e-115;
 Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2496 agtctgactggaagctgaagctcagatcgaatctggaactgctctataaccat 2535
 DB 500 agtctgactggaagctgaagctcagatcgaatctggaactgctctataaccat 441
 QY 2556 ttcccccctgttttaagagctccaaatgctcagaataaggaacattgcaataag 2615
 DB 440 ttcccccctgttttaagagctccaaatgctcagaataaggaacattgcaataag 381
 QY 2616 ctgattttttaaagctcatttccctcttaagctcttcaagctccttcaaaagac 2675
 DB 380 ctgattttttaaagctcatttccctcttaagctcttcaagctccttcaaaagac 321
 QY 2676 agaatactgatttctgataattttagtgcttaagcattccaaatataaggaacaca 2735
 DB 320 agaatactgatttctgataattttagtgcttaagcattccaaatataaggaacaca 261
 QY 2736 aaatccaggaatgcqgttagcttaaccctcttcccatcggaacagctcctacac 2795
 DB 260 aaatccaggaatgcqgttagcttaaccctcttcccatcggaacagctcctacac 201
 QY 2796 aaatttaagaatgctcgtttaccacaaatgctgcatatgattgtgtatgattaca 2855
 DB 200 aaatttaagaatgctcgtttaccacaaatgctgcatatgattgtgtatgattaca 141
 QY 2856 caggaatctctgcaagctgcaagaagatctcctaaacgggaaggaaggaatgaa 2915
 DB 140 caggaatctctgcaagctgcaagaagatctcctaaacgggaaggaaggaatgaa 81
 QY 2916 cctccttactgtgacccctcccaaaactagctcagtgcaaggtatacagtgctcatt 2975
 DB 80 cctccttactgtgacccctcccaaaactagctcagtgcaaggtatacagtgctcatt 21
 QY 2976 aaattctgataatca 2993
 DB 20 aaattctgataatca 3
 RESULT 4
 A1372923 471 bp mRNA EST 16-FEB-1999
 LOCUS q299a05.q1 Soares_Pregnant_Uterus_NbHPU Homo sapiens cDNA clone
 DEFINITION IMAGE:2048672 3', mRNA sequence.
 ACCESSION A1372923
 VERSION A1372923.1 GI:4152789
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

QY 3218 ggtgcatcatgttagatcttcttgagagtgaaacacccctgcccctcacaataacagagc 3277
 DB 423 GAGGATATCATGTTAGATTTCTTGAGAGTGAAAACACCTGCCATCAAAATTAACAAGG 364
 QY 3278 tggataacagctcactccacttgaattcaagtgaagaccccaagctaggtcttactga 3337
 DB 363 TGGATTAACAGCTCCTCCATTTGAAATTCAGTGAACCCAAAGCTAGGTTCTTACTGA 304
 QY 3338 attgatactcaatttgggaaactgaacttagcttcaaaagctcagaagcttggtg 3397
 DB 303 ATTGATCTCAATTTGGGAAACTGAACTTAGCTTTCAAAAGATCAATGAAAGTCTGTTG 244
 QY 3398 gagaacactagagatctctctgcaatggtgaggaagagtggtcagaataacccagctgc 3457
 DB 243 GAGAAACTAGGAGATTTTCGCGAATGGCGAGAGAGGTGTCAGAAATTAACCACTGCC 184
 QY 3458 catgtgtttgagaacacgaactatctatgcagagccggagggaagctcacaaccca 3517
 DB 183 CATGCTTTTGAAGAAACGGAACATCTTATGACAGACCCCGAGGCAAGCTCAAAACCCA 124
 QY 3518 tgggttgaagccatgaggaaggaatttgatccaatgtaatgaactcttcttaagta 3577
 DB 123 TGGCTTGAAGCCATGAGAGAAATTTGATCAATGTAATGAACCTCTTTAACTCA 64
 QY 3578 gaattccctgcacatggtgtgctgattcaataaaataaagaataataataatg 3637
 DB 63 GAATTTCCCTGCAATGCTGTGCGCTGATTCATTAATAATTAATAATTAATG 4
 QY 3638 aag 3640
 DB 3 AAA 1

RESULT 8
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 DEFINITION mRNA sequence.
 ACCESSION BE350495
 VERSION BE350495.1 GI:9262348
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 417)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
 Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov
 Seq primer: -40UP from Gbco
 High quality sequence stop: 414.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3146713"
 /clone_1lb="NCI_CGAP_Kid13"
 /tissue_type="2 pooled Wilms' tumors, one primary and one
 metastatic to brain"
 /lab_host="DH10B"

BASE COUNT 143 a 82 c 64 g 128 t
 ORIGIN
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 Site_2: NotI; Cloned unidirectionally. Primer: Oligo df.
 Library constructed by Life Technologies."
 Query Match 11.4%; Score 415.4; DB 107; Length 417;
 Best Local Similarity 99.8%; Pred. No. 5e-95;
 Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 417 ACTTAATAAGGTTTAAAGCTGAAGAGTGAAGCTCAAGAAAGGTTGTTGAATG 358
 QY 2276 aatataagctcttatttcttgattaggaataataattactgtagaatcttt 2335
 DB 357 AATATCAGCTATATATTTATTTAGTGAATAATAATTAATTAATTAATTTCTT 298
 QY 2336 attagagcttctctgctcagacatgctcctcaagcttgatgataagctcagct 2395
 DB 297 ATTAGAGGCTTTTCTGTCGACACATTTCTCAGTGTTCATGATTAAGTCTACG 238
 QY 2396 aatctacgacaatgttgaagaagttcccaattatttctgcttacaatgtgaac 2455
 DB 237 AATCTTACAGACATTTGAGAAAGTCCCATATATTTCTGTTTACAAATGTGAAC 178
 QY 2456 ggaagctctatagagtggaagaaactcaaccagatcaccagttgtgctggaagtt 2515
 DB 177 GGAAGCTCATAGAGTGGAAGAACTCAACAGAGTACCAGTGTGACTGGAAAGTT 118
 QY 2516 agattcagatcgaattgactgctcttataaccatacttcccccgttttagagc 2575
 DB 117 AGGATTCAGATCGAAATTTGAGCTGCTTTATTAACCATATTTTCCCGCTTTTAGAC 58
 QY 2576 ttccaaatgttcgaataaggaacatgtcacaataaagcttgatttttaagtc 2632
 DB 57 TTCCAATGTGCAGATGAGAAACATTCATAAATGAGCTGATTTTATATGC 1

RESULT 9
 AM804917 406 bp mRNA EST 16-MAY-2000
 LOCUS OV4-UM0094-280300-152-h08 UM0094 Homo sapiens cDNA, mRNA sequence.
 DEFINITION AM804917
 ACCESSION AM804917.1 GI:7856696
 VERSION AM804917.1 GI:7856696
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 406)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Cavallho, A.F., Matsukuma, A., Bais, G.S., Simpson, D.H.,
 Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.C.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 200202663
 COMMENT
 CONTACT: Simpson A.J.C.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Paraf. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the RAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?el=OV4-UM0094-280>)

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
ATTHONS	1 (bases 1 to 381)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdnp/image/image.html Seq primer: M13 Forward POLYA=yes.
FEATURES	Location/Qualifiers
SOURCE	1..381 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2724153" /clone_lib="NCI-CGAP_Sub4" /lab_host="DH10B (Life Technologies)" /note="Vector: pYT3D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The NCI-CGAP Sub4 library is a subtracted library derived from the NCI-CGAP Sub2 library which is a subtracted library derived from the NCI-CGAP Sub1 library, which is a subtracted library derived from B1. B1 constitutes a mixture of 21 normalized or subtracted NCI-CGAP libraries: NCI-CGAP_C04, NCI-CGAP_P122, NCI-CGAP_P128, NCI-CGAP_C010, NCI-CGAP_C016, NCI-CGAP_R105, NCI-CGAP_R1012, NCI-CGAP_R103, NCI-CGAP_R1011, NCI-CGAP_Lym2, NCI-CGAP_Br2, NCI-CGAP_C08, NCI-CGAP_CLL1, NCI-CGAP_Le12, NCI-CGAP_Br23, NCI-CGAP_Lu5, NCI-CGAP_Lu24, NCI-CGAP_Lu19, NCI-CGAP_G04, NCI-CGAP_GC6, NCI-CGAP_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI-CGAP_R103 pool 1 : L1AM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids 1322376-1323911, 1456008-1456775, 1500552-1502855) NCI-CGAP_R105 pool 1 : L1AM 3338-3343, 3722-3725, 3776-3778 (IMAGE Clonoids 1322912-1325831, 1471368-1472903, 1492104-1493255) NCI-CGAP_Lu5 pool 1 : L1AM 3575-3582, 3851-3854 (IMAGE Clonoids 1414920-1417991, 1520504-1522433) NCI-CGAP_G04 pool 1 : L1AM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI-CGAP_P122 pool 1 : L1AM 2457-2459, 2758-2759, 3063-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615) NCI-CGAP_C010 pool 1 : L1AM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145355) Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery Genome Research 6, 791-806.] TAG_LIB=NCI-CGAP_C010 TAG_TISSUE=colon TAG_SEQ=AAACG"
BASE COUNT	97 a 104 g 103 t
ORIGIN	97 a 104 g 103 t
Query Match	9.5%; Score 348.2; DB 88; Length 381;
Best Local Similarity	98.9%; Pred. No. 6.7e-78;
Matches 361; Conservative	0; Mismatches 3; Indels 1; Gaps 1;

Db	381	GCACCAATGAACCTTACACACTTGGGGTTGGATGACGACAGCGCTCTATCAACCCCAAGTA	322
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Db	321	CTGTGAGGTTGTCATATGACAAATAGTGTCTGCATCCCTACAAAGCTTAAGACTATGACAGT	262
QY	866	gtctctccagtgcttcgatgtggtctgtctctcccgccaggtctctatgataatgctg	925
Db	261	GTCTCTCCAGTGCTCTGATGTGGCTGTGCTCTCTCCGCGAGTCTCTATGATTAATGCTTG	202
QY	926	ctctctgaacctgtgactgttagaatacccaatgacatcttctgacttgatctctacc	985
Db	201	CTTCTGTAACTGTAGCTGTAGGAATCCCAATGAATCTTTGTCTACTTTGGATCTTACCC	142
QY	986	tgactcttcagaatctgccaaactaggaagacacaaatcttggtctcttgaggactaacca	1045
Db	141	TGACTCTTCAGAAATGTGCACACTAGGACAGGACAAATCTTGCTTGAGGAGTAACCA	82
QY	1046	atgcctcttgagagcagtgtagcccttaatgagccataactttaccacaatgagccttagttac	1105
Db	81	ATGCGCTGGAAGCAGTACAGCCCTTATGGCCAAATCTTTCACCAATGAGCGCTTAGTTAC	22
QY	1106	ccctga	1110
Db	21	CTCTGA	17.

RESULT 12

LOCUS A0726685

DEFINITION HS_3411_B2_H02_17A RPCI-11 Human Male BAC Library Homo sapiens genomic Clone Plate-987 Col-4 Row=P, DNA sequence.

ACCESSION A0726685

VERSION A0726685.1

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 503)

AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

MEDLINE 99380589

COMMENT Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallaceu.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@ejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.hnsc.washington.edu

Seq primer: 17

Plate: 987, Row: P, Column: 4

Class: BAC ends

High quality sequence stop: 503.

FEATURES

Source

1..503

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/db_xref="taxon:9606"

/clone="plate-987 Col-4 Row=P"

/clone_id="RPCI-11 Human Male BAC Library"

/sex="male"

note=Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;

Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
 Seq primer: -400p from Gibco.

FEATURES

Source

1. 320
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="2479007"
 /clone_lib="NCI-CGAP_GC6"
 /tissue_type="Pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Plasmid DNA from the normalized library NCI-CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1257096-1258631, 1469064-1470983, and 1475392-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

102 a 58 c 56 g 104 t

ORIGIN

Query Match 8.2%; Score 300; DB 27; Length 320;
 Best Local Similarity 100.0%; Pred. No. 1.3e-65;
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2329 tctcttattttagggccttctgtccagacatctcagtgcttgatgcatgattg 2388
 Db 320 tctcttattttagggccttctgtccagacatctcagtgcttgatgcatgattg 261
 QY 2389 ctcaactgaatcttcagacaatgttgaagatccattattctgttctacaat 2448
 Db 260 ctcaactgaatcttcagacaatgttgaagatccattattctgttctacaat 201
 QY 2449 gtgaacggaagctcagatagatgtgaagaaactcaaccagatgcttgatgcatgattg 2508
 Db 200 gtgaacggaagctcagatagatgtgaagaaactcaaccagatgcttgatgcatgattg 141
 QY 2509 gaaagttagatcagatcagatggaatgttcttataaccattttcccccgttt 2568
 Db 140 gaaagttagatcagatcagatggaatgttcttataaccattttcccccgttt 81
 QY 2569 tttagagcttccaagtgtcagatagagaagaacattgcaataaagtgtgattttttaa 2628
 Db 80 tttagagcttccaagtgtcagatagagaagaacattgcaataaagtgtgattttttaa 21

RESULT 15

AA316760 311 bp mRNA EST 19-APR-1997
 DEFINITION EST18843 Lung Homo sapiens cDNA 5' end, mRNA sequence.
 ACCESSION AA316760
 VERSION AA316760.1 GI:1969089
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 311)
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulcher,R.A., Bult
 C.J., Lee,N.H., Kirschner,E.F., Weinschenk,K.G., Gocayne,J.D., White
 O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Val,C., Clayton,R.A.,

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
 L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodex,A.,
 Guelm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
 Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
 Small,R.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
 Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
 Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
 Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
 Wei,Y.F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillion,P.J., Fannon
 M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
 Venter,J.C.

TITLE

Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence

JOURNAL

Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE

96026280

COMMENT

Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
 Seq primer: M3 Reverse.

FEATURES

Source

1. 311
 /organism="Homo sapiens"
 /db_xref="ATCC (host):117430"
 /db_xref="taxon:9606"
 /clone_lib="Lung"
 /dev_stage="adult"
 /note="Organ: Lung; Vector: pBluescript SK-; Site_1: EcoRI
 Site_2: XhoI"

BASE COUNT

101 a 54 c 58 g 96 t 2 others

ORIGIN

Query Match 8.1%; Score 295.4; DB 5; Length 311;
 Best Local Similarity 98.7%; Pred. No. 1.9e-64;
 Matches 307; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 2833 atgaatgttgatgattatccaggaatctcgtcagtgatgagagatctctaa 2892
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 QY 2893 cgggaagagatggaatatacctccttactgtgacctcccaaacctagtcagt 2952
 Db 61 cgggaagagatggaatatacctccttactgtgacctcccaaacctagtcagt 120
 QY 2953 caagatatacagtggtgccattataactgatatgatacaggaacgtgtgcatgttc 3012
 Db 121 caagatatacagtggtgccattataactgatatgatacaggaacgtgtgcatgttc 180
 QY 3013 ctactttatcgaagctctctcttccaaagctacatagaataatttaacagta 3072
 Db 181 ctactttatcgaagctctctcttccaaagctacatagaataatttaacagta 240
 QY 3073 aaatttataatagtgcttcgaaagagacattata-ttcaagaatgtcatat 3131
 Db 241 aaatttataatagtgcttcgaaagagacattataatattttcaagaatgtcatat 300
 QY 3132 gtaagatata 3192
 Db 301 gtaagatata 311

Search completed: February 25, 2001, 15:20:31

Mon Feb 26 08:43:32 2001

us-09-325-019-1.rst

Page 12

Job time: 29172 sec


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Db 1440 tggagctctctcgtccagagccctgacccctctccgagaggggtctaaagctctcgga 1499
QY 439 actgctgtgagcagtggtgtgtgtgagacgacgacagagagccacgacagacccccc 498
Db 1500 aatgctcggaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1559
QY 499 gtgcacacagagccctctgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 552
Db 1560 tccggtctcagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1619
QY 553 gcatagctcacaagacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 612
Db 1620 gccgtgtccagagccacagaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1679
QY 613 ctccgagctccaaatgttaacgcccagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 672
Db 1680 cccggtgtacacaaatgtacacagccctctcgacgtgtgtgtgtgtgtgtgtgtgtgtgt 1739
QY 673 tgcggcactgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 732
Db 1740 tcaagctctgtgagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1799
QY 733 tgtaccagccagagagctacacacacacacacacacacacacacacacacacacacac 792
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QY 793 atcaacccaagtagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 852
Db 1860 accgagctcaaaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1919
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QY 913 ggaatgaatgctgtctctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 972
Db 1980 tcaataagactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2039
QY 973 tggaaatccactgactctcagaaatgtgcaactagagcagagcacaatctgtgtgtc 1030
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RESULT 2
US-09-054-274-1
Sequence 1, Application US/09054274
Patent NO. 6150101

GENERAL INFORMATION:

APPLICANT: University of South Florida
APPLICANT: Grodenorst, Gary R.
APPLICANT: Bradham, Jr., Douglas M.
TITLE OF INVENTION: METHODS OF IDENTIFYING A COMPOSITION
TITLE OF INVENTION: THAT ALTERS CONNECTIVE TISSUE GROWTH
TITLE OF INVENTION: FACTOR EXPRESSION (Amended)
FILE REFERENCE: 07414/003004
CURRENT APPLICATION NUMBER: US/09/054, 274
CURRENT FILING DATE: 1998-04-02
EARLIER APPLICATION NUMBER: 08/386, 680
EARLIER FILING DATE: 1995-02-10
EARLIER APPLICATION NUMBER: 08/459, 717
EARLIER FILING DATE: 1995-06-02
EARLIER APPLICATION NUMBER: 08/167, 628
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2970
TYPE: DNA

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; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1025)...(2074)
US-09-054-274-1

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Query Match 6.7%; Score 246.4; DB 3; Length 2998;
Best Local Similarity 54.7%; Pred. No. 1.3e-50;
Matches 524; Conservative 12; Mismatches 410; Indels 12; Gaps 3;

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QY 82 caccocgtctccgcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 141
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QY 142 ggcgtccagcgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 201
Db 1203 ggcgcacaaagcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1262
QY 202 tctactgtgactacagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 261
Db 1263 tctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1319
QY 262 tccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 321
Db 1320 atgtgtctctctcgtacatctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1379
QY 322 accgcaagagtaacacacacacacacacacacacacacacacacacacacacacacacac 378
Db 1380 gctgcagagctccagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1439
QY 379 tccgagtgcccccgcgcgtctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 438
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QY 439 actgctgtgagcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 498
Db 1500 aatgctcggaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1559
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QY 553 gcatagctcacaagacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 612
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QY 793 atcaacccaagtagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 852
Db 1860 accgagctcaaaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1919
QY 853 agactatcgagctgtctctcagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 912
Db 1920 ccaaccccgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1979
QY 913 ggaatgaatgctgtctctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 972
Db 1980 tcaataagactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2039
QY 973 tggaaatccactgactctcagaaatgtgcaactagagcagagcacaatctgtgtgtc 1030

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Db      2040  tgaactacaggaagtgtaacggaacatgagcatgahelunereunyrryrgsetcyllys 2057

RESULT      3
US-08-167-628-1
: Sequence 1, Application US/08167628
: Patent No. 5408040
:
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
:
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: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2075 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: IMMEDIATE SOURCE:
: CLONE: DB60R32
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 130..1177
:
US-08-167-628-1

Query Match      6.7%; Score 243.4; DB 1; Length 2075;
Best Local Similarity 56.2%; Pred. No. 5,8e-50;
Matches 523; Conservative 0; Mismatches 396; Indels 12; Gaps 3

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Oy      142  ggcgtcacgagcttgaggagcaactgaagagagctgcactctgtgtgaccccaacggggacc 201
Db      308  GCGCAACAGACGTGGCGGCGAGCTGTGACCGAGCGCACCCCTGTGCGACCCGCGACAGAGGCC 367
Oy      202  tctactgtgactacagcgggagccgcgcgaagtaacgaatgagtgctgtgaagatgtg 261
Db      368  TCTTGTGTGACT---TCGGCTTCCCGGCGCCAACCGCAAGATCGGCGGTGTGCACCGCCAAAG 424
Oy      262  tgggtgtggcgtgcgtccctggatggggtgcgttacaacaagcgcagtcctcttcacagccta 321
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[illegible]


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Query Match          6.7%: Score 243.4; DB 1; Length 2075;
Best Local Similarity 56.2%: Pred. No. 5, 8e-50;
Matches 523; Conservative 0; Mismatches 396; Indels 12; Gaps 3

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QY      142  ggcctcagacagcttggggaaacactgcagggagctgtgcaattgtgaacccacggggcc 201
DB      308  GGGCCAGACAGCTGGGGCGAGCTGTGCACACGACGGGACCCCTGTGCGACCCGACAAAGGCC 367

QY      202  tctactgtgactcaacaggcgggagacgcgcccaggtagtgcgaatgaagatgtgtgaacaggtg 261
DB      368  TCTTGTGTGACT---TCGGCTCCCGGGCCACACCGCAAGATCGGCGTGTCTACCGCCAAAG 424

QY      262  tcgggtgtggctgctgtcctgtgaatgggtgtgcgtacaaacaaacggcgcaagtccttcagccta 321
DB      425  ATGGAGTCTCCCTCGACATCTTCGGGTGGAGCGGTATACCGCAGCGGAGAGTCTCTTCAGAGCA 484

QY      322  actgcaagtatacactgcgcacgtgtcatcgaacggcggtgtggctgtgcacacacgtt---gcc 378
DB      485  GCTGCAAGATACCAATGACAGTGCCTGTGGAAGGGGGCGGTGGCTGACAGCCCTGTGCAAGCA 544

QY      379  tcggagtgcgccccccgctctctgtgtgcgcccaacggcgggcggtgtgaatatacctgtgcc 438
DB      545  TGGAGCTTCTGTGCTGCTGCCACAGCCTGTACTGCCCTTCCCGAGAGGGGTCAAGCTGTCCGGGA 604

QY      439  actgctgtgagcagttggtatgtatgagagcaagcgaagagccgaacgcaagccgcaacccc 498
DB      605  AATGCTGGGAGAGATGGGGGTGTGTGACAGCCCAAGAGCAAAACCGGTGTGGGGCTGTGCC 664

QY      499  gtgacaacggagacctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 552
DB      665  TCGCGGCTTACCGACTGGAAGACAGCTTTGGCCCAACCCCAACTATGATTAGACCAACT 724

QY      553  gcatgacctatacaagccccctggagcgcccttgcctgtccacacggcgctgggggtctctca 612
DB      725  GCGTGTGTCAGACACACAGATGGAGGGCGCTGTTCCAAGACCTGTGGAGATGGGCATTTCCA 784

QY      613  ctcgagatctccaatgtltaacgcccagctgtgcctgtgacgaagagagcgccctctgaact 672
DB      785  CCCGGGTACCAATGACAGCGCTCCTCGAGGCTAGAGAAAGCAGAGCCCGCTGTGCATGG 844

QY      673  tgcggccatgtcgatgtgagcatccatcacactcattaaaggcaaggaaagtgtctgtcg 732
DB      845  TCAGGCTTTGCAAGACTGTGACTGTGAAGAGAAATTTAAGAAAGGCCAAAAAGTGATCCGTA 904

QY      733  tgtacacgacgagagcatcatcgtaaactcaacactctgcgctgcgcatcagcaacgctct 792
DB      905  CTCGCCAAATATCTCCAAAGCCTATCAAGTTTGAGCTTTCTGTGCTGCACACACATGAAACAT 964

QY      793  atcaaacccaagtaactgtgtgagtttgcataygacaataatgtgtctgtcatccctcaaatcta 852
DB      965  ACCGAGCTAAATTTCTGTGAGATATGATACCGAGCGGCGGATGTGCACCCCGCCACAGAAACA 1024

QY      853  agacatacgagctgtccctccagttgcgctgcgatagggttggcttctcccgccaggtctcat 912
DB      1025  CCACCGTCCGGGTGAGATTCAAGTGCCCTGACGGCGCAGGTCAATGAAGAAACATATATGT 1084

QY      913  ggaattaatgcctgtctctgttaacctgagctgtgagaaatcccaatgacatcttgcgact 972
DB      1085  TCATCAAGACACGTGTGCTCTCCATTTAAACATGTGCCGAGACAAATGACATCTTTGATTCG 1144

QY      973  tggaaatcctaaccttgacttctcaagaattgc 1003
DB      1145  TGTACTACAGAAAGATGTACGGAGACATGGC 1175

RESULT      6
US-08-712-302-1
: Sequence 1, Application US/08712302

```

```

Patent No.5783187
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,302
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
US-08-712-302-1

Query Match          6.7%: Score 243.4; DB 1; Length 2075;
Best Local Similarity 56.2%; Pred. No. 5,8e-50;
Matches 523; Conservative 0; Mismatches 396; Indels 12; Gaps 3

QY      82 caaccctgcgtccgcttggcggtcacaagtcacatgaatgctgttgatgctgtaagaatgt 141
DB      248 CGCCCGCGGCGGCCGGCGGCAGCTTCGTGTAACGCGTGGCGGCTGTCGCCGCGTCT 307
QY      142 ggcgtcacgacgcttctggggaacaactcaaggaagctgcacatctgttaaccaccaagggcc 201
DB      308 GCGCCAAACAGCTGGGCGGCGAGCTGCACCAGCACGCGACCCCTGCGACCCGCAACAAGGGCC 367
QY      202 tctactgtgacctaacaggcgggagccgcggaggtagcaatagagttgttgtacaagttgg 261
DB      368 TTTTGTTGACT--TCGGCTCCCGCGCCAACCCGAAGATCGCGGTGTGCACCGCCAAG 424
QY      262 tcgggtgtggctgcgccttcctgatactgggtgctgtacaaacaagcgcaagtccttcacagcta 321
DB      425 ATGGAGTCCCTCGCATCTTCGGTGGTAGCGGTATACCGCAAGAGAGTCTTCCAGAGCA 484
QY      322 actgcaagtcatcaactgcacgtgatcatcagcgcgggtgggtggtgacacacacattgt---gcc 378

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Db 485 GCTGCAAGTACGACGACGCTGCTGAGCGGGCGGTGGCTGCATGCCCTGTGCACGA 544
Qy 379 tccagatgcgccccgcgctctctgtgtccccccacgcgcgcgtgagatcacctggcc 438
Db 545 TGAGAGTCTGTGCTCCAGAGCCCTGACTGCCCCCTTCCCGAGAGAGGTCAACCTGCCGGGA 604
Qy 439 acgtcgtgtgcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 438
Db 605 AATGCTGCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 664
Qy 499 gtgacacagagagccttcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 552
Db 665 TCCGGGCTTACCGACTGGAAGACAGCTTTGGCCAGACCCAACTATATTAGAGCCACT 724
Qy 553 gcatagctacacagagcccttgagccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 612
Db 725 GCTGTGTCAGACCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 764
Qy 613 ctgcgacttccatgtttaagcccgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 672
Db 785 CCGGGGTACCAATGACACAGCCCTCTGCAAGGCTAGAGAGAGAGAGAGAGAGAGAGAGAG 844
Qy 673 tgcggccatgcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 732
Db 845 TCAGGCTTTCGAAAGCTGACTGTGAAGAGACATTAAAGAGGCAAAAGTGCATCCGTA 904
Qy 733 tgtaaccagagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 792
Db 905 CTCCTCAAAATCTCCAAAGCTTATCAAGTTTGTGAGCTTTCTGTGCTGCACCAAGATGACAT 964
Qy 793 atcaacccaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 832
Db 965 ACCGAGTAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1024
Qy 853 agcatcagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 912
Db 1025 CCACCGTCCGGGTGAGATTCAAGTCCCTGACGCGAGGTCAAGAAAGAACTGTATGT 1084
Qy 913 ggaattatgcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 972
Db 1085 TCATCAAGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1144
Qy 973 tgaatcctacccctgacttctcagaattgc 1003
Db 1145 TGTACTACAGAAAGATGTACGAGACATGCG 1175

```

RESULT 7
US-08-880-031-1
Sequence 1, Application US/08880031
Patent No. 5916736

GENERAL INFORMATION:
APPLICANT: Grotenborst, Gary R.
APPLICANT: Bradham Jr., Douglas M.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,031

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US/08/167,628
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: DB60R12
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
US-08-880-031-1

Query Match 6.7%; Score 243.4; DB 2: Length 2075;
Best Local Similarity 56.2%; Pred. No. 5,8e-50;
Matches 523; Conservative 0; Mismatches 396; Indels 12; Gaps 3;

Qy 82 caccgcctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 141
Db 248 CGCGGCGCTGCCCCGGGGGCGTGAAGCTGTGTGAACGCTGCGCTGCTGCGCTGCTGCGCTG 307
Qy 142 ggcctcagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 201
Db 308 GCGCCAGACAGTGGGCGAGAGCTGTGACCAAGGCGGACCCCTGACACCGACCAAGAGGCC 367
Qy 202 tctactgtgactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 261
Db 368 TCTTCTGTGTACT--TGGCTCCCGCGCCAAACCGAAGATCGCGTGTGACCGCCAAAG 424
Qy 262 tgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 321
Db 425 ATGCTGCTCCCTGCTCATCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 484
Qy 322 actgcagatcaaacctgcagctgcagctgcagctgcagctgcagctgcagctgcagctgc 378
Db 485 GCTGCAAGTACGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 544
Qy 379 tccagatgcgccccgcgctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 438
Db 545 TGAGAGTCTGTGCTCCAGAGCCCTGACTGCCCCCTTCCCGAGAGAGGTCAACCTGCCGGGA 604
Qy 439 acgtcgtgtgcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 498
Db 605 AATGCTGCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 664
Qy 499 gtgacacagagccttcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 552
Db 665 TCCGGGCTTACCGACTGGAAGACAGCTTTGGCCAGACCCAACTATATTAGAGCCACT 724
Qy 553 gcatagctacacagagcccttgagccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 612
Db 725 GCTGTGTCAGACCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 764
Qy 613 ctgcgacttccatgtttaagcccgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 672
Db 785 CCGGGGTACCAATGACACAGCCCTCTGCAAGGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 844
Qy 673 tgcggccatgcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 732
Db 845 TCAGGCTTTCGAAAGCTGACTGTGAAGAGACATTAAAGAGGCAAAAGTGCATCCGTA 904
Qy 733 tgtaaccagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 792

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Db 905 CTCGCAAAATCTCCAGCCTATCAAGTTTGAGCTTCTGCTGCACACAGCAATGAAGACAT 964
 Qy 793 atcaaccgaagctggtgagttgcatgagacaatagtgctgcatccctcaagctca 852
 Db 965 ACCGAGCTAAATCTGTGAGATGATACAGCGCGGATGTCACACCCCAAGAACCA 1024
 Qy 853 agactatcagctgtctccctcagctgctgcatgagctgtgcttcccgccagctcat 912
 Db 1025 CCACCTGCGGGTGGAGTTCAAGTCCCTGACGCGGAGTCAATGAAGAATCATGATGT 1084
 Qy 913 ggattaatgctgtctgtctgtaacctgagctgtagaataccaatgacatcttgcgact 972
 Db 1085 TCATCAAGACCTGTGCTGCTCCATTCATCACTGTCCGAGACATGACATCTTGAATCGC 1144
 Qy 973 tggatccctaccctgactctcagaatgtgc 1003
 Db 1145 TGTACTACGAGAAGATGTACGAGACATGCG 1175

RESULT 8

US-09-097-179-1

Sequence 1, Application US/09097179

Patent No. 6149916

GENERAL INFORMATION:

APPLICANT: Grotendorst, Gary R.

APPLICANT: Bradham Jr., Douglas M.

TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Spensley Horn Judas & Lubitz

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,179

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/386,680

FILING DATE: 10-FEB-1995

APPLICATION NUMBER: US/08/167,628

FILING DATE:

APPLICATION NUMBER: US/07/752,427

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Wetherell, Jr. Ph.D., John W.

REGISTRATION NUMBER: 31,678

REFERENCE/DOCKET NUMBER: PD-1294

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-455-5100

TELEFAX: 619-455-5110

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2075 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: DB60R32

FEATURE:

NAME/KEY: CDS

LOCATION: 130..1177

US-09-097-179-1

Query Match 6.7%; Score 243.4; DB 3; Length 2075;
 Best Local Similarity 56.2%; Pred. No. 5.8e-50;
 Matches 523; Conservative 0; Mismatches 396; Indels 12; Gaps 3;

Qy 82 caaccgcctgcccgtggtggtgagctcctacacagatgctgtgagctgtgtaagatgt 141
 Db 248 CCGCCGCTGCGCCCGCGGGCGGAGCTGCTGAGAGCGGCTGCTGAGAGCGGCTGCTGCT 307
 Qy 142 ggcctcagcagctgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 201
 Db 308 GCGCAAGAGCTGGGCGAGCTGCTGAGAGCGGAGCTGCTGAGAGCGGAGCTGCTGAGAG 367
 Qy 202 tctactgtgactacagcgggagcggcggcggcggcggcggcggcggcggcggcggcggc 261
 Db 368 TCTTCTGTGACT---TCGGCTCCCGGCGCAACCGCAAGTCCGCTGTCCAGAGCAAG 424
 Qy 262 tcggtgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 321
 Db 425 ATGAGCTCCCTGCACTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 484
 Qy 322 actgcaagtacacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 378
 Db 485 GCTGCAAGTACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 544
 Qy 379 tcgaggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 438
 Db 545 TGGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 604
 Qy 439 actgctgtgagcagctggtggtggtggtggtggtggtggtggtggtggtggtggtggt 498
 Db 605 AATGCTGCGAGAGTGGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 664
 Qy 499 gtgacacagagcctcgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgt 552
 Db 665 TCGCGGCTTACCGAGTGAAGACAGTGTGCGCCAGACCACTATGATTAAGCCAACT 724
 Qy 553 gtagacctaacaagcccttgagcccttgagcccttgagcccttgagcccttgagcccttgag 612
 Db 725 GCTGTGCTCAGACACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 784
 Qy 613 ctcgagatcacaatgttaacgcccagctgctgctgctgctgctgctgctgctgctgctgct 672
 Db 785 CCGGGTTACCAATGACAAAGCTGCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 844
 Qy 673 tgcggccatgctgtgagcatcctacatcattaaaggcaggaagagagagagagagag 732
 Db 845 TCAGGCTTGCAGAGCTGACCTGGAAGAGACATTAAAGAGGCAAAAAGTGCATCCGTA 904
 Qy 733 tglacagcagaagcatcagaactcaacacttggtggtggtggtggtggtggtggtggt 792
 Db 905 CTCGCAAAATCTCCAGCCTATCAAGTTTGAGCTTCTGCTGCACACAGCAATGAAGACAT 964
 Qy 793 atcaaccgaagctggtgagttgcatgagacaatagtgctgcatccctcaagctca 852
 Db 965 ACCGAGCTAAATCTGTGAGATGATACAGCGCGGATGTCACACCCCAAGAACCA 1024
 Qy 853 agactatcagctgtctccctcagctgctgcatgagctgtgcttcccgccagctcat 912
 Db 1025 CCACCTGCGGGTGGAGTTCAAGTCCCTGACGCGGAGTCAATGAAGAATCATGATGT 1084
 Qy 913 ggattaatgctgtctgtctgtaacctgagctgtagaataccaatgacatcttgcgact 972
 Db 1085 TCATCAAGACCTGTGCTGCTCCATTCATCACTGTCCGAGACATGACATCTTGAATCGC 1144
 Qy 973 tggatccctaccctgactctcagaatgtgc 1003
 Db 1145 TGTACTACGAGAAGATGTACGAGACATGCG 1175

RESULT 9

PCT-US96-08140-1

Sequence 1, Application PC/TUS9608140

```

GENERAL INFORMATION:
APPLICANT: University of South Florida
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08140
FILING DATE: 30-MAY-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07414/003WO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: CTGF
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
PCT-US96-08140-1

Query Match      6.7%; Score 243.4; DB 4; Length 2075;
Best Local Similarity 56.2%; Pred. No. 5.8e-50;
Matches 523; Conservative 0; Mismatches 396; Indels 12; Gaps 3;

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QY 499 gtgacacaggagcctcgatgctggtgaggtgagcaltgacacagga-----act 552
DB 665 TCGCGGCTTACGAGCTGGAAGACAGTTGGCCAGACCACTATGATTAGACCAACT 724
QY 553 gcatgagctacacagcccttgagcccttgctccacccagcggcctgggggtctcca 612
DB 725 GCGTGTCCAGACACAGAGTGAAGCGCTGTCCAGACCTGTGGATGGCATCTCCA 784
QY 613 ctggaatcccaatgttaagcccaagtgctggcctgagcaagagacgcctcgcaact 672
DB 785 CCGGGTTACCAATGACAAAGCCTCTCGAGGCTAGAGAGAGAGAGCCCTGTGATGG 844
QY 673 tgcgagcaltgagatgtgacatccatcaactaatgaaggcaggaaaggtctggctg 732
DB 845 TAGAGCGCTTGCAGAGCTGTGACCTGGAAGAAACATTTAGAGAGGCAAAAAGTCATCCGA 904
QY 733 tgtacagccagagagatccatcaactcaacttgccggtcgatccagcaagcctct 792
DB 905 CTGCCAAAATCTCCAAAGCTATCAAGTTGAGCTTCTGAGTCAACCACTAGAGACAT 964
QY 793 atcaaccacagatctgtgaggttgatgacatagtgatgcatccctacagtgta 852
DB 965 ACCGAGCTAAATTTCTGTGAGATATGACGAGCGCGGATGCTGCAACCCCAAGACCA 1024
QY 853 agacatcgagtgctctccagtgctcgtatggcttgcttcgccaggtctcat 912
DB 1025 CCACCTGCCGGGTGAGTCAAGTGCCCTGACGCGAGCGAGCTCATGAGAGAAACATGATGT 1084
QY 913 ggtatattgcctgctctgttaacatgagctgtgagaaatccaatgacatcttgagct 972
DB 1085 TCATCAAGACTGTGCTCCATTTACAACTGTCCCGAGACAAATACATCTTTGAATCCG 1144
QY 973 tggatccctaacctgactctccagaaatgac 1003
DB 1145 TGTACTACAGAAAGATGTACGAGACATGGC 1175

RESULT 10
US-08-459-101A-1
Sequence 1, Application, 'us/08459101A
Patent No. 5945300.
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Connective Tissue Growth Factor-2
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: CAPILLA, BYRNIE, BAIN, GILFILLAN,
ADDRESSER: CROCHT, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,101A
FILING DATE: June 2, 1995
CLASSIFICATION: 356
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07736
FILING DATE: 12 JUL 94
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-317
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

```

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
US-08-459-101A-1

Query Match 2.8%; Score 102.2; DB 2; Length 1128;
Best Local Similarity 53.0%; Pred. No. 9.9e-16;
Matches 218; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 548 gaactgatatgctaccacgaagcccttgagccctgtctccacagctgagccgctgggt 607
DB 684 GAATGATGTTCAACAACTTCATGCTCCAGTCTCAAGACCTGTGGAACCTGGTAT 743
QY 608 ctccactgcatctccatgttaacgcagctgctgagcgaagagagccgctctg 667
DB 744 CTCACACGAGTACCAATACAACTGATGCTGCGCTTGTGAAGAAACCGGATTTG 803
QY 668 caactgagccatgagatgtgacatcatcaatcaatcaagcaggaagaagtgtct 727
DB 804 TGAGGTGCGGCTTGTGAGACGACGCTGACAGCAGCTGAAAAAGGGCAAGAAATGAC 863
QY 728 gactgtgtaccagccagagcatccatgaactcacactgagcggctgacacagcag 787
DB 864 CAGACCAAGAAATCCCGCCAGACGACGAGTTACTACGCTGAGTGTGAGTGA 923
QY 788 ctccatcaacacagatgtgagttgcatgacatagttgctcatccctcaaa 847
DB 924 GAATACGGGCCCAAGTACGCTGCTTCTGCTGAGAGCGCGATGCTGACGCCCGCAGCT 983
QY 848 gtctaagactatgagcgtgctctccagttccctgattggcctgctcccgccaggt 907
DB 984 GACCAGCAGCTGTGAAGATGGGCTCCCTCGCAGAGTGGGAGACATTTTCAAGAACGT 1043
QY 908 ccatgattaatagcgtctctgttaaccctgagctgagtgtaagaatcccatga 958
DB 1044 CATGATGATCAGTCTTCAAAATGCACTACACTGCCCGCATGCCAARGA 1094

RESULT 11
US-08-656-393-1
Sequence 1, Application US/08656393

GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
TITLE OF INVENTION: METHODS AND USES OF CONNECTIVE TISSUE
TITLE OF INVENTION: GROWTH FACTOR AS AN INDUCTION AGENT
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,393
FILING DATE: 31-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-040
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2541 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-656-393-1

Query Match 1.6%; Score 57.8; DB 2; Length 2541;
Best Local Similarity 68.6%; Pred. No. 8.9e-05;
Matches 94; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY 82 caccgcctgacccgctgggggtcagcctcatcacagatgctgtgagctgtaaatgt 141
DB 2101 CGCGGGGCTGCGCGGGGGGGGTGAGCCTGCTGTGAGAGGCTGCGGCTGCGCGGTCT 2160
QY 142 ggcctcagcagctgggggacactgcagagagctgcatctgtgacccacagggcc 201
DB 2161 GCGC-AAGCAGCTGGCGGAGCTGTGACGACGAGCGACCCCTGCGACCGACAGAGGCC 2219
QY 202 tctactgtgactcagc 218
DB 2220 TCTTCTGTGACTTGGC 2236

RESULT 12
US-08-117-373-7/C
Sequence 7, Application US/08117373

GENERAL INFORMATION:
APPLICANT: BOWDEN, PAUL E.
APPLICANT: LUC, XIAOCHUN
APPLICANT: MAMRYZYNAK, CYNTHIA J.
TITLE OF INVENTION: ISOLATED HAIR KERATIN GENES AND THEIR
TITLE OF INVENTION: USE IN HAIR GROWTH ACTIVE IDENTIFICATION ASSAYS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE PROCTER & GAMBLE COMPANY
STREET: 11810 EAST MIAMI RIVER ROAD
CITY: CINCINNATI
STATE: OHIO
COUNTRY: USA
ZIP: 45239-8707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,373
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONSTANDE, BRAHM J.
REGISTRATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 4518R26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-2858
TELEFAX: (513) 627-2858
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-117-373-7

[illegible]

Db 27223 TTTAAAGTATTCCTTATTAATCTGCAGCAAGCTCATAGAGCTTTTATTTATTT 27282
QY 2288 ttcttattgtattagaaataataattactgttagaattctttatttgggacct 2347
Db 27283 TATTTTATTTTTCCTTTTACACAGATATATTAACACAAACATTTGTTGTTTC 27342
QY 2348 ttctgtgcagacattgctctcagtgcttgcattgattagctcactgaattctcagac 2407
Db 27343 CTGTGACACAGCTCTGTGTGTAAGCACTTAACAT-CACATATATCAAGCACTTTGCTAAT 27401
QY 2408 aatgttgagaagttcccatattattctgttcttacaatgtgaaagcgaagctatag 2467
Db 27402 AAGCTGTGAATAATGATATTAATTTCTGCTTT--ACAGCTGCAACAGAGACTCAGAG 27458
QY 2468 aggtgagaaactcaaccagagtcaccagcttg 2501
Db 27459 AGGTTAGTAACTTGCCCGAGTCAAGAGACTGG 27492

RESULT 15

US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-F1s
US-08-232-463-14

QY 885 gggcttgctctcccgccaggtccatgatgaatagctgctctgtaacctgagctgt 944
Db 1035 GAGCTTGCTGCGAGCTGAGGAGCTTGCGATTTTTTTTTTTTTTTTTTTTTT 1094
QY 945 aggaatcccaatgacatctctgtctgacttgaaatccatccctgactctcagaatggc 1004
Db 1095 YY 1154
QY 1005 aactagcgagcaaatcttggtctctgggaactaacccaatgctgtgaagcagtcag 1064
Db 1155 YY 1214
QY 1065 cccctatggcgaataactcttccacaaatgagcccttagtaacctgactgagaccctggc 1124
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QY 1125 ctccattctgtctgaacatccaatgacgctgattgtctgctcagggccatgcta 1184
Db 1275 YY 1334
QY 1185 tgagtttctccttgatcatcattcagcatctactcctaagaaaatgctgtctcagct 1244
Db 1335 YY 1394
QY 1245 gtcttgactacacccagccttgatcagccttccaaatcagtaagtcctcctgctgat 1304
Db 1395 YYGNACAAATCTCTATCTC 1454
QY 1305 ctgcttaaatcccaagaatgaaatca 1332
Db 1455 TTTAACTACTTGATAGATAGTAAATTA 1482

Search completed: February 25, 2001, 16:36:27
Job time: 23368 sec

Query Match 1.2%; Score 45.2; DB 1; Length 7218;
Best Local Similarity 8.5%; Pred. No. 0.16;
Matches 38; Conservative 211; Mismatches 199; Indels 0; Gaps 0;

